



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 173123

TO: Ruixiang Li
Location: REM/4D75/4C70
Art Unit: 1646
Thursday, December 15, 2005
Case Serial Number: 10/061727

From: Kristine Hensle
Location: Biotech-Chem Library
REM-1B69
Phone: (571) 272-4161

Kristine. Hensle@uspto.gov

Search Notes

Examiner Li,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Kristine Hensle
Librarian
STIC Biotech/Chem Library
(571)272-4161

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From: Li, Ruixiang
Sent: Thursday, December 01, 2005 4:04 PM
To: STIC-Biotech/ChemLib
Subject: Sequence search of Application No.10/061,727

Please do a standard search on:

- (i).SEQ ID NO: 2 against interference amino acid databases;
(ii). SEQ ID NOS: 1 and 2 against interference nucleic acid databases.

Thank you very much!

Ruixiang Li
GAU 1646
REM 4D75
Mail Box 4C70
(571) 272-0875

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STIC/BIOTECH LIBRARY
(STIC)

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 14, 2005, 07:35:54 ; Search time 377 Seconds
(without alignments)
9731.796 Million cell updates/sec

Title: US-10-061-727-1
Perfect score: 2064
Sequence: 1 atgacactctctggtgtgtg.....acgacttttatacctataa 2064

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 88878028 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*

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3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
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8: /cgn2_6/ptodata/1/ina/RE COMB.seq.*
9: /cgn2_6/ptodata/1/ina/backfilee1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1388.4	67.3	1740	3	US-08-991-944-1
2	1388.4	67.3	4724	3	US-09-949-016-313
3	1388.4	67.3	4726	3	US-09-949-016-5448
4	1073	52.0	2703	3	US-10-282-162-39
5	1073	52.0	2709	3	US-10-282-162-41
6	1073	52.0	2709	3	US-10-282-162-43
7	1069.6	51.8	2748	3	US-10-282-162-51
8	1069.6	51.8	2754	3	US-10-282-162-53
9	1069.6	51.8	2754	3	US-10-282-162-55
10	1069.2	51.8	2733	3	US-09-313-942-27
11	1069.2	51.8	2733	3	US-10-282-162-27
12	1067.4	51.7	3355	3	US-08-991-944-3
13	1017	49.3	2703	3	US-10-282-162-33
14	1017	49.3	2709	3	US-10-282-162-35
15	1017	49.3	2709	3	US-10-282-162-37
16	1015	49.2	2748	3	US-10-282-162-45
17	1015	49.2	2754	3	US-10-282-162-47
18	1015	49.2	2754	3	US-10-282-162-49
19	292.8	14.2	141454	3	US-09-949-016-12055
20	292.8	14.2	141455	3	US-09-949-016-17190
21	235.8	11.4	601	3	US-09-949-016-24207
22	235.8	11.4	601	3	US-09-949-016-190484
23	153.8	7.5	601	3	US-09-949-016-24225
24	153.8	7.5	601	3	US-09-949-016-190530

25	151	7.3	2061	3	US-09-173-151A-3	Sequence 3, Appli
26	149.8	7.3	601	3	US-09-949-016-24226	Sequence 24225, A
27	149.8	7.3	601	3	US-09-949-016-190531	Sequence 190531, A
28	149.4	7.2	601	3	US-09-949-016-24224	Sequence 24224, A
29	149.4	7.2	601	3	US-09-949-016-190515	Sequence 190515, A
30	144.4	7.0	2537	3	US-09-173-151A-34	Sequence 34, Appli
31	139.4	6.8	1737	3	US-09-173-151A-1	Sequence 1, Appli
32	96	4.7	229	3	US-09-513-999C-11178	Sequence 13178, A
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34	89.6	4.3	1626	3	US-09-110-618-1	Sequence 1, Appli
35	89.6	4.3	1626	3	US-09-578-178-1	Sequence 1, Appli
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40	88	4.3	3522	3	US-09-023-655-906	Sequence 906, App
41	88	4.3	3522	3	US-09-949-002-74	Sequence 74, Appl
42	88	4.3	3522	3	US-09-949-002-203	Sequence 203, App
43	75.2	3.6	1563	3	US-08-996-338-1	Sequence 1, Appli
44	75.2	3.6	1563	3	US-09-556-972-1	Sequence 1, Appli
45	75.2	3.6	1620	3	US-08-996-338-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-08-991-944-1
; Sequence 1, Application US/08991944
; Patent No. 6280955
; GENERAL INFORMATION:
; APPLICANT: Cao, Zhaoan
; TITLE OF INVENTION: Interleukin-1 Receptor Accessory Proteins,
; TITLE OF INVENTION: Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 75 DENISE DRIVE
; CITY: HILLSBOROUGH
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94010
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/991,944
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-014
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 343-4341
; TELEFAX: (650) 343-4342
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1740 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 10..1719
US-08-991-944-1

Query Match 67.3%; Score 1388.4; DB 3; Length 1740;
Best Local Similarity 89.6%; Pred. No. 0;
Matches 1517; Conservative 0; Mismatches 171; Indels 6; Gaps 2;

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QY 10 ATGACACTCTGTGGTGTGTAGTGTCTCTACTTTTATGGAACTCTGCAAGTGTATGCC 69
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QY 61 TCAGAACGCTGGCATGACTGGGAGCTAGACACATGAGGCAAAATCAAGTGTGGAAGAT 120
DB |||||
QY 70 TCAGAACGCTGGCATGACTGGGAGCTAGACACATGAGGCAAAATCAAGTGTGGAAGAT 129
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QY 130 GAGCCAGCTCGCATCAAGTGGCCACTCTTTGAACTCTTGAACACTCTTGAATTTCAACTACAGCACA 189
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DB |||||
QY 190 GCCCATTTAGCTGGCCCTTACTCTGATCTGTGTTTGGACTAGGACGACCGGACCTTGTAG 249
DB |||||
QY 241 GAGCCAAATTAATTCGCCCTCCCGAGAAACCGCATTTAGTAAAGGAGAAAGATGTGCTGTGG 300
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QY 301 TTCCGGCCCACTCTCTCAATGACACTGGCACTATACCTGCATGTTAAAGGACACTACA 360
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QY 310 TTCCGGCCCACTCTCTCAATGACACTGGCACTATACCTGCATGTTAAAGGACACTACA 369
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QY 430 CCATGAATCTCCAGTGCATAACTGTTATATAGAAATATGGCAATTCAGAGGATCACTGT 489
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QY 481 CCATGAATCTCCAGTGCATAACTGTTATATAGAAATATGGCAATTCAGAGGATCACTGT 540
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QY 1021 GTTGCCAAAGCAGCCAAAGGTGAAGCAAGAAAGTGCAGCTCCAAAGATACACAGTGAAGCTG 1080
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QY 1090 GCTTGTGGTTTTGGAGCCACAGTCTCTGCTAGTGTGATTTCTCATTTGTTTACCATGTT 1149
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QY 1261 GTATTACTGACCCCTCCGTTGGAGTTTTGGAGAAATGAATTTGGATACAAGCTGTGCATCTTT 1320
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QY 1321 GACCGAGACAGTCTGCTGGGGGAAATACAGTGGGAAGCAGTTTTTTGATTTCAATTCAGAGA 1380
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QY 1441 CTGAGAGTTTAAACTGGGTGTCAATGTGCCAGAACTCCATTTG---CCACCAAGCTCATTTGTG 1497
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QY 1510 GTACAGTCAAAAGCTGTGAAAGGAAACGAAAGGTGAAAGAGCTGAAGAGGGCTAAGACGGTG 1569
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QY 1615 GCTTGTGGTTGGCTCTTCCCTGTGAAAGTCTGAGTGGCCAGTTCTGGCTGGAATGAGAGC 1674
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QY 1630 CAGCTGCAGGTGGCCATGCCAGTGAAGAAAGTCCAGGCGGTCTAGCAGTGTGATGAGCAG 1689
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QY 1690 GGCCTCTCGTATT 1703
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RESULT 2

US-09-949-016-313
; Sequence 313, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 313
; LENGTH: 4724
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-313

Query Match 67.3%; Score 1388.4; DB 3; Length 4724;
Best Local Similarity 89.6%; Pred. No. 0; Mismatches 171; Indels 6; Gaps 2;
Matches 1517; Conservative 0

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DB 207 ATGACACTTCTGTGTGTGTAGTGAAGTCTCTACTTTTATGGAATCCTGCAAGTGATGCC 266
QY 61 TCAGAACGCTGCGATGACTGGGAGTAGACACCAATGAGGCAATCCAAAGTGTGTAAGAT 120
DB 267 TCAGAACGCTGCGATGACTGGGAGTAGACACCAATGAGGCAATCCAAAGTGTGTAAGAT 326
QY 121 GAGCCAGCTCGCATCAAGTGCCCACTCTTTGAAACACTTTTGAATTCACACTACAGACA 180
DB 327 GAGCCAGCTCGCATCAAGTGCCCACTCTTTGAAACACTTTTGAATTCACACTACAGACA 386
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DB 387 GCCCATTCAAGTGGCCCTTACTCTGATCTGGTATTTGGAAGTGGAGGACCGGACCTTTGAG 446
QY 241 GAGCCAAATTAATTCGCGCTCCCGGAGAACCGCAATTAAGAGGAAAGATGTGCTGTGG 300
DB 447 GAGCCAAATTAATTCGCGCTCCCGGAGAACCGCAATTAAGAGGAAAGATGTGCTGTGG 506
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QY 361 TATTGAGCAAAAGTTGCATTTCCCTTGGAAAGTTGTTCAAAAAGACAGCTGTTTCAATTCC 420
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QY 541 TGTATATAAATACAGAAATTTTAAATGTAATACCGGAAGGTATGAATTTGAGTTTCCCTC 600
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QY 661 CGTACGTTTTCATCTCACCAGGACTCTGACTGTAAGGTAGTAGGCTCTCCAAAATGCA 720
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QY 721 GTGCCCCCTGTGATCCATTCACTATGATCATGTGCTCTATGAGAAAGAACCCAGGAGAG 780
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DB 987 GAGCTACTCATTCCTGTACGGTCTATTTAGTTTCTGATGATTTCTCGCAATGAGTTT 1046
QY 841 TGGTGACCAATTGATGGAAGAAACCTGATGATGATCACTTATGATGTCACCATTAACGAA 900
DB 1047 TGGTGACCAATTGATGGAAGAAACCTGATGATGATCACTTATGATGTCACCATTAACGAA 1106
QY 901 AGTATAAGTCATAGTAGAAGAGTGAACCAAGAACTCAGATTTTGGAGCTCAAGAAA 960
DB 1107 AGTATAAGTCATAGTAGAAGAGTGAACCAAGAACTCAGATTTTGGAGCTCAAGAAA 1166
QY 961 GTTACCTCTGAGATCTCAAGCGCAGCTATGTCTGCTAGTAAGAGTCCAAAGCGCAA 1020
DB 1167 GTTACCTCTGAGATCTCAAGCGCAGCTATGTCTGCTAGTAAGAGTCCAAAGCGCAA 1226
QY 1021 GTTGCCAAAGCGCAGCTGAGCAAGAGTGGCCAGCTCCCAAGATACACAGTGGNACTG 1080
DB 1227 GTTGCCAAAGCGCAGCTGAGCAAGAGTGGCCAGCTCCCAAGATACACAGTGGNACTG 1286

QY 1081 GCTTGTGGTTTTGGAGCCACAGTCTCTAGTGGTGAATCTCATTTGTTTGTACCATGTT 1140
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DB 1347 TACTGGCTAGAGATGTCCTATTTTACCGGGCTCAATTTTGGAAACAGATGAAACCATTTTA 1406
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DB 1407 GATGGAAAGAGATGATGATATTTATGATATCTTATGATATCTTATGCAAGGAATCGGAAGAGAAATTT 1466
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DB 1527 GACCGAGAGATGTCCTGGGGGAAATGTACAGATGAGACTTTTGAGCTTCATTCAGAAA 1586
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DB 1587 AGCAGAGAGATGATTTGTTCTGAGCCCTGACTATGTGACAGAAAAGACATCAGCATG 1646
QY 1441 CTGGAGTTTTAACTGGGTGTCTATGTCAGAACTCCATTTG---CCACCAAGCTCATTTGTG 1497
DB 1647 CTGGAGCTCAAGCTGGCTAGAAATATGGCTCTCGGGGCAACATCAACGTCATTTTA 1706
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DB 1707 GTACAGTACAAAGCTGTGAAGGAAACGAAGGTGAAAGAGCTGAAGGGCTAAAGACGGTG 1766
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QY 1615 GCTTTCGGTGGCTCTTCCCTCGAGAGTCTGAGTGCCAGATTTCTGGCTGGAATGAGAGC 1674
DB 1827 CAGCTGACAGTGGCCATGCCAGTGAAGAAAGTCCAGCGGGTCTAGCAGTGATGAGCAG 1886
QY 1675 TGCCTCTTCCAGTTC 1688
DB 1887 GGCCTCTCGTATTC 1900

RESULT 3

US-09-949-016-5448
; Sequence 5448, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5448
; LENGTH: 4726
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-5448

Query Match 67.3%; Score 1388.4; DB 3; Length 4726;
Best Local Similarity 89.6%; Pred. No. 0;
Matches 1517; Conservative 0; Mismatches 171; Indels 6; Gaps 2;

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QY 1 ATGACACTTCTGTGTGTGTAGTGTAGTCTCTACTTTATGGAATCCTGCAAAAGTGATGCC 60
Db |||
QY 207 ATGACACTTCTGTGTGTGTAGTGTAGTCTCTACTTTATGGAATCCTGCAAAAGTGATGCC 266
Db |||
QY 61 TCAGAACGCTGCGATGACTGGGGACTAGACACATGAGGCAAAATCAAGTGTGGAAGAT 120
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QY 267 TCAGAACGCTGCGATGACTGGGGACTAGACACATGAGGCAAAATCAAGTGTGGAAGAT 326
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QY 181 GCCCATTCAGCTGGGCTTACTCTGTATCTGTATGAGCTAGGACGACCGGACCTTGAG 240
Db |||
QY 387 GCCCATTCAGCTGGGCTTACTCTGTATCTGTATGAGCTAGGACGACCGGACCTTGAG 446
Db |||
QY 241 GAGCCAAATTAATTCGCGCTCCCGAGAACCCGATTTAGTAAGGAGAAAGATGTGCTGTGG 300
Db |||
QY 447 GAGCCAAATTAATTCGCGCTCCCGAGAACCCGATTTAGTAAGGAGAAAGATGTGCTGTGG 506
Db |||
QY 301 TTCCGGCCCACTCTCTCAATGACACTGGCACTATACCTGATGTTAAGGAACACTACA 360
Db |||
QY 507 TTCCGGCCCACTCTCTCAATGACACTGGCACTATACCTGATGTTAAGGAACACTACA 566
Db |||
QY 361 TATTGAGCAAAAGTTGCAATTCCTTGGAAAGTTGTTCAAAAAGACAGCTGTTCAATTCC 420
Db |||
QY 567 TATTGAGCAAAAGTTGCAATTCCTTGGAAAGTTGTTCAAAAAGACAGCTGTTCAATTCC 626
Db |||
QY 421 CCCATGAACCTCCAGTGATGATTAATGATGATATAGAAATGCGATTTAGGAGATCACTGT 480
Db |||
QY 627 CCCATGAACCTCCAGTGATGATTAATGATGATATAGAAATGCGATTTAGGAGATCACTGT 686
Db |||
QY 481 CCAATGTAGTGGATATTTCTCCAGTGTCACAGCTGTCACAGCTATCATTGTTGATATGGC 540
Db |||
QY 687 CCAATGTAGTGGATATTTCTCCAGTGTCACAGCTGTCACAGCTATCATTGTTGATATGGC 746
Db |||
QY 541 TGTATATAAATACAGAAATTTTAAATGTAATACCCGAGGTATGAACTTGAGTTTCTCTC 600
Db |||
QY 747 TGTATATAAATACAGAAATTTTAAATGTAATACCCGAGGTATGAACTTGAGTTTCTCTC 806
Db |||
QY 601 ATTGCTTAAATTTCAAAATGGAATTAACATGTTGTTTACATATCCAGAAAATGGA 660
Db |||
QY 807 ATTGCTTAAATTTCAAAATGGAATTAACATGTTGTTTACATATCCAGAAAATGGA 866
Db |||
QY 661 CGTAGCTTTTCATCTCACCAGGACTCTGACTGTAAGGTAGTAGGCTCTCCAAAATGCA 720
Db |||
QY 867 CGTAGCTTTTCATCTCACCAGGACTCTGACTGTAAGGTAGTAGGCTCTCCAAAATGCA 926
Db |||
QY 721 GTGCCCCCTGTGATCCATTACCTAATGATCATGTGGTCTATGAGAAAGAACCCAGGAG 780
Db |||
QY 927 GTGCCCCCTGTGATCCATTACCTAATGATCATGTGGTCTATGAGAAAGAACCCAGGAG 986
Db |||
QY 781 GAGTACTCATTTCCCTGTACGGTCTATTTTGTGTTTCTGATGGATTCGCAATGAGTT 840
Db |||
QY 987 GAGTACTCATTTCCCTGTACGGTCTATTTTGTGTTTCTGATGGATTCGCAATGAGTT 1046
Db |||
QY 841 TGGTGGACCATTTGATGGAAGAAACCTGATGATCATCACTATTGATGTCACCAATTAACGA 900
Db |||
QY 1047 TGGTGGACCATTTGATGGAAGAAACCTGATGATCATCACTATTGATGTCACCAATTAACGA 1106
Db |||
QY 901 AGTATAAGTCATAGTAGAACAGAAATGAAACAGAACTCAGATTTTGGAGCATCAAGAAA 960
Db |||
QY 1107 AGTATAAGTCATAGTAGAACAGAAATGAAACAGAACTCAGATTTTGGAGCATCAAGAAA 1166
Db |||
QY 961 GTTACTCTGAGGATCTCAAGCGAGCTATGTCTGTCTAGTGTAGAGTGCACAAAGCGAA 1020
Db |||
QY 1167 GTTACTCTGAGGATCTCAAGCGAGCTATGTCTGTCTAGTGTAGAGTGCACAAAGCGAA 1226
Db |||
QY 1021 GTTGCCAAAGCAGCAGGAGTGAAGCAGAAAGTGCAGCTCCCAAGATACACAGTGAACCTG 1080
Db |||
QY 1227 GTTGCCAAAGCAGCAGGAGTGAAGCAGAAAGTGCAGCTCCCAAGATACACAGTGAACCTG 1286
Db |||
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QY 1081 GCTTGTGGTTTTGGAGCCACAGTCTCTGTAGTGGTGAATCTCATTTGTTGTTTACCATGTT 1140
Db |||
QY 1287 GCTTGTGGTTTTGGAGCCACAGTCTCTGTAGTGGTGAATCTCATTTGTTGTTTACCATGTT 1346
Db |||
QY 1141 TACTGGCTAGAGATGGTCTCTATTTTACCGGGCTCATTTTGGAAACAGATGAACCAATTTA 1200
Db |||
QY 1347 TACTGGCTAGAGATGGTCTCTATTTTACCGGGCTCATTTTGGAAACAGATGAACCAATTTA 1406
Db |||
QY 1201 GATGAAAAGAGTATGATATTTATCTATCTATCAAGAAATGCGGAAGAAGAAATTT 1260
Db |||
QY 1407 GATGAAAAGAGTATGATATTTATCTATCTATCAAGAAATGCGGAAGAAGAAATTT 1466
Db |||
QY 1261 GTATTACTGACCCCTCCGTGGAGTTTTTGGAGAAATGAATTTGGATACAAAGCTGTGCATCTTT 1320
Db |||
QY 1467 GTATTACTGACCCCTCCGTGGAGTTTTTGGAGAAATGAATTTGGATACAAAGCTGTGCATCTTT 1526
Db |||
QY 1321 GACCAGACAGTCTGCTGGGGGAAATACAGTGGGAAGCAATTTTGTATTTCAATTCAGAGA 1380
Db |||
QY 1527 GACCAGACAGTCTGCTGGGGGAAATTTGTACAGATGAGACTTTTGAGCTTTCATTCAGAAA 1586
Db |||
QY 1381 AGCAGAAAGATGATTTGTTTCTGAGCCCTGACTATGTGACAGAAAAGAGCATCAGCATG 1440
Db |||
QY 1587 AGCAGACGCTCTGCTGGTTTCTAAGCCCCCACTAGTGTCCAGGGAACCCAGCCCTC 1646
Db |||
QY 1441 CTGGAGTTTAAACTGGGTGTCATGTGCCAGAACTCCATTTG---CCACCAAGCTCATTTGTG 1497
Db |||
QY 1647 CTGGAGCTCAAGGCTGGCTAGAAAATATGGCTCTCGGGGCAACATCAACGTCATTTTA 1706
Db |||
QY 1498 GTTGTGTACGCTCCCTTGTAGCACCCGACCCAGGCATTTCTCAGCTCAAGAGCTGTG 1557
Db |||
QY 1707 GTACAGTACAAAGCTGTGAAGGAAACGAAGGTGAAAGAGCTGAAGAGGGCTAAGACGGTG 1766
Db |||
QY 1558 ---TCCTTTGTGAGCTGGAAGGAGAAAGTCCAAACATCTCGGCTCTATAATTTTGGAAA 1614
Db |||
QY 1767 CTCAGGCTATTAATGGAAGGGGAAATCCAAAGTATCCACAGGGCAGGTTCTGGAG 1826
Db |||
QY 1615 GCTTTGCGGTTGGCTCTTCCCTGAGAAAGTCTGAGTGGCAGTTCTGGCTGGAATGAGAGC 1674
Db |||
QY 1827 CAGCTGCAAGTGGCCATGCCAGTGAAGAAAAGTCCAGGCGGTCTAGCAGTGTAGAGCAG 1886
Db |||
QY 1675 TGCTCTTCCAGTC 1688
Db |||
QY 1887 GGCCTCTCGTATTC 1900
Db |||
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RESULT 4

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US-10-282-162-39
; Sequence 39, Application US/10282162
; Patent No. 6927044
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; TITLE OF INVENTION: AND USING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282,162
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 39
; LENGTH: 2703
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-282-162-39
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Query Match 52.0%; Score 1073; DB 3; Length 2703;
Best Local Similarity 97.8%; Pred. No. 0;
Matches 1088; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
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QY 1 ATGACACTTCTGTGTGTGTAGTGTAGTCTCTACTTTTATGGAATCCTGCAAAAGTGATGCC 60
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1 ATCGTCTCTGTGTGTAGTCTCTACTTTATGGAATCTCGCAAGTGATGCC 60
61 TCAGAACGCTGCGATGACTGGGACTAGACACCATGAGGCAAAATCCAAAGTGTGGAAGAT 120
61 TCAGAACGCTGCGATGACTGGGACTAGACACCATGAGGCAAAATCCAAAGTGTGGAAGAT 120
121 GAGCCAGCTCGCATCAAGTCCCACTCTTTGAACTCTTTGAAATTTCAACTACAGCACA 180
121 GAGCCAGCTCGCATCAAGTCCCACTCTTTGAACTCTTTGAAATTTCAACTACAGCACA 180
181 GCCCATTACGCTGGCCTTACTCTGATCTGCTGATTTGGACTAGGAGGACCGGACCTTGAG 240
181 GCCCATTACGCTGGCCTTACTCTGATCTGCTGATTTGGACTAGGAGGACCGGACCTTGAG 240
241 GAGCCAAATTAACCTTCGCGCTCCCGAGAACCGCATTTAGTAAGGAGAAAGATGCTGTGG 300
241 GAGCCAAATTAACCTTCGCGCTCCCGAGAACCGCATTTAGTAAGGAGAAAGATGCTGTGG 300
301 TTCGGGCCCACTCTCTCAATGACACTGGCAACTATACCTGCAATGTTAAGGAACACTACA 360
301 TTCGGGCCCACTCTCTCAATGACACTGGCAACTATACCTGCAATGTTAAGGAACACTACA 360
361 TATTGACGCAAAAGTTGCATTTCCCTTGGAAAGTTGTTCAAAAAGACAGCTGTTTCAATTC 420
361 TATTGACGCAAAAGTTGCATTTCCCTTGGAAAGTTGTTCAAAAAGACAGCTGTTTCAATTC 420
421 CCATGAAACTCCAGTGCAATAAATCTGATATATAGAAATATGCAATGATGATGATGATG 480
421 CCATGAAACTCCAGTGCAATAAATCTGATATATAGAAATATGCAATGATGATGATGATG 480
481 CCAAAATGATAGATGGAATATTTTCTCCAGTGTCAAAACCGCATATCACTTGGTATATGG 540
481 CCAAAATGATAGATGGAATATTTTCTCCAGTGTCAAAACCGCATATCACTTGGTATATGG 540
541 TGTGTTAAAAATACAGAAATTTTAAATGTAATGTAATGTAATGTAATGTAATGTAATG 600
541 TGTGTTAAAAATACAGAAATTTTAAATGTAATGTAATGTAATGTAATGTAATGTAATG 600
601 ATTGCGCTTAAATTTCAAAATATGGAATTTTAAATGTAATGTAATGTAATGTAATGTA 660
601 ATTGCGCTTAAATTTCAAAATATGGAATTTTAAATGTAATGTAATGTAATGTAATGTA 660
661 CGTACCTTTTCATCTCACCAGGACTCTGACCTGTAAGGCTAGTGGCTCTCCAAAATGCA 720
661 CGTACCTTTTCATCTCACCAGGACTCTGACCTGTAAGGCTAGTGGCTCTCCAAAATGCA 720
721 GTGCCCCCTCTGATCCATTCACCTAATGATCATGTGCTCTATGAGAAAGAACCCAGGAG 780
721 GTGCCCCCTCTGATCCATTCACCTAATGATCATGTGCTCTATGAGAAAGAACCCAGGAG 780
781 GAGCTACTCATTCCTCTGACGGTCTATTTTGTGTTTCTGATGATGATGATGATGATGAT 840
781 GAGCTACTCATTCCTCTGACGGTCTATTTTGTGTTTCTGATGATGATGATGATGATGAT 840
841 TGTGTGACCATTCATGGAAGAAACCTGATGATGATGATGATGATGATGATGATGATGAT 900
841 TGTGTGACCATTCATGGAAGAAACCTGATGATGATGATGATGATGATGATGATGATGAT 900
901 AGTATAAGTCATAGTAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
901 AGTATAAGTCATAGTAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
961 GTTACCTCTGAGATCTCAAGCCAGCTATGCTGCTGATGATGATGATGATGATGATGATG 1020
961 GTTACCTCTGAGATCTCAAGCCAGCTATGCTGCTGATGATGATGATGATGATGATGATG 1020
1021 GTTGCCAAAGCAGCCAGGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
1021 GTTGCCAAAGCAGCCAGGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
1081 GCTTGTGTTTGGAGCCACAGTCTCTGCTAGTG 1113
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Db 1081 TGCAAGGAACGTGAAGAAAAATAATTTTAGTG 1113
RESULT 5
US-10-282-162-41
; Sequence 41, Application US/10282162
; Patent No. 6927044
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; TITLE OF INVENTION: AND USING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282,162
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 41
; LENGTH: 2709
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-282-162-41
Query Match 52.0%; Score 1073; DB 3; Length 2709;
Best Local Similarity 97.8%; Pred. No. 0;
Matches 1088; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
QY 1 ATGACACTTCTGTGGTGTGTAGTACTCTACTTTTATGGAATCTCTGCAAAAGTGATGCC 60
Db 1 ATGCGTCTTCTGTGGTGTGTAGTACTCTACTTTTATGGAATCTCTGCAAAAGTGATGCC 60
QY 61 TCAGAACGCTGCGATGACTGGGACTAGACACCATGAGGCAAAATCCAAAGTGTGGAAGAT 120
Db 61 TCAGAACGCTGCGATGACTGGGACTAGACACCATGAGGCAAAATCCAAAGTGTGGAAGAT 120
QY 121 GAGCCAGCTCGCATCAAGTCCCACTCTTTGAACTCTTTGAAATTTCAACTACAGCACA 180
Db 121 GAGCCAGCTCGCATCAAGTCCCACTCTTTGAACTCTTTGAAATTTCAACTACAGCACA 180
QY 181 GCCCATTACGCTGGCCTTACTCTGATCTGCTGATTTGGACTAGGAGGACCGGACCTTGAG 240
Db 181 GCCCATTACGCTGGCCTTACTCTGATCTGCTGATTTGGACTAGGAGGACCGGACCTTGAG 240
QY 241 GAGCCAAATTAACCTTCGCGCTCCCGAGAACCGCATTTAGTAAGGAGAAAGATGCTGTGG 300
Db 241 GAGCCAAATTAACCTTCGCGCTCCCGAGAACCGCATTTAGTAAGGAGAAAGATGCTGTGG 300
QY 301 TTCGGGCCCACTCTCTCAATGACACTGGCAACTATACCTGCAATGTTAAGGAACACTACA 360
Db 301 TTCGGGCCCACTCTCTCAATGACACTGGCAACTATACCTGCAATGTTAAGGAACACTACA 360
QY 361 TATTGACGCAAAAGTTGCATTTCCCTTGGAAAGTTGTTCAAAAAGACAGCTGTTTCAATTC 420
Db 361 TATTGACGCAAAAGTTGCATTTCCCTTGGAAAGTTGTTCAAAAAGACAGCTGTTTCAATTC 420
QY 421 CCCATGAAACTCCAGTGCAATAAATCTGATATATAGAAATATGCAATGATGATGATGATG 480
Db 421 CCCATGAAACTCCAGTGCAATAAATCTGATATATAGAAATATGCAATGATGATGATGATG 480
QY 481 CCAAAATGATAGATGGAATATTTTCTCCAGTGTCAAAACCGCATATCACTTGGTATATGG 540
Db 481 CCAAAATGATAGATGGAATATTTTCTCCAGTGTCAAAACCGCATATCACTTGGTATATGG 540
QY 541 TGTGTTAAAAATACAGAAATTTTAAATGTAATGTAATGTAATGTAATGTAATGTAATG 600
Db 541 TGTGTTAAAAATACAGAAATTTTAAATGTAATGTAATGTAATGTAATGTAATGTAATG 600
QY 601 ATTGCGCTTAAATTTCAAAATATGGAATTTTAAATGTAATGTAATGTAATGTAATGTA 660
Db 601 ATTGCGCTTAAATTTCAAAATATGGAATTTTAAATGTAATGTAATGTAATGTAATGTA 660
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QY 661 CGTACGTTTCATCTCACAGGACTCTGACTGTAAAGGTAGTAGGCTCTCAAAAAATGCA 720
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Db 661 CGTACGTTTCATCTCACAGGACTCTGACTGTAAAGGTAGTAGGCTCTCAAAAAATGCA 720
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QY 721 GTGCCCCCTGTGATCAATTCACCTAATGATCATGTGGTCTATGAGAAAGAACCCAGAGAG 780
| | | | |
Db 721 GTGCCCCCTGTGATCAATTCACCTAATGATCATGTGGTCTATGAGAAAGAACCCAGAGAG 780
| | | | |
QY 781 GAGTACTCATTCCTCTGACGGTCTATTTTCTGATGATTCGCAATGAGTT 840
| | | | |
Db 781 GAGTACTCATTCCTCTGACGGTCTATTTTCTGATGATTCGCAATGAGTT 840
| | | | |
QY 841 TGGTGGACCATTTGATGGAAAAAACCCTGATGACATCACTATTGATGTCAACCAATCAAGAA 900
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Db 841 TGGTGGACCATTTGATGGAAAAAACCCTGATGACATCACTATTGATGTCAACCAATCAAGAA 900
| | | | |
QY 901 AGTATAAGTCATAGTAGAAACAGAGATGAAACAGAACTCAGATTTTGAGCATCAAGAAA 960
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Db 901 AGTATAAGTCATAGTAGAAACAGAGATGAAACAGAACTCAGATTTTGAGCATCAAGAAA 960
| | | | |
QY 961 GTTACTCTGAGGATCTCAAGCGCAGCTATGTCTGTCTAGTAGAGTCCCAAGCGGAA 1020
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Db 961 GTTACTCTGAGGATCTCAAGCGCAGCTATGTCTGTCTAGTAGAGTCCCAAGCGGAA 1020
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QY 1021 GTTGCCAAAGCAGCCAAAGGTGAAGCAGAAAGTGCCAGCTCCCAAGATGCAAGTGA 1080
| | | | |
Db 1021 GTTGCCAAAGCAGCCAAAGGTGAAGCAGAAAGTGCCAGCTCCCAAGATGCAAGTGA 1080
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QY 1081 GCTTGTGTTTTGGAGCCACAGCTCTGCTAGTG 1113
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Db 1081 TGCAAGGAACGTGAAGAAAAATAATTTTAGTG 1113
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RESULT 6

US-10-282-162-43
; Sequence 43, Application US/10282162
; Patent No. 6927044
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282,162
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 43
; LENGTH: 2709
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-282-162-43

Query Match 52.0%; Score 1073; DB 3; Length 2709;
Best Local Similarity 97.8%; Pred. No. 0;
Matches 1088; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 1 ATGACACTTCTGTGTGTAGTAGTCTCTACTTTTATGGAATCCTGCAAGTAGTGCC 60
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Db 1 ATGGTGCTTCTGTGTGTAGTAGTCTCTACTTTTATGGAATCCTGCAAGTAGTGCC 60
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QY 61 TCAGAACGCTGCGATCACTGGGGACTAGACACCATGAGCAATCCAGTGTGTAAGAT 120
| | | | |
Db 61 TCAGAACGCTGCGATCACTGGGGACTAGACACCATGAGCAATCCAGTGTGTAAGAT 120
| | | | |
QY 121 GAGCAGCTGCGATCAAGTGCCCACTCTTTGAACTCTTCTGAAATTCAACTACAGCACA 180
| | | | |
Db 121 GAGCAGCTGCGATCAAGTGCCCACTCTTTGAACTCTTCTGAAATTCAACTACAGCACA 180
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RESULT 7

US-10-282-162-51
; Sequence 51, Application US/10282162
; Patent No. 6927044
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282,162
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 43
; LENGTH: 2709
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-282-162-51

QY 181 GCCCATTCAGCTGGCGCTTACTCTGTATTTGGATTTGGACTAGGACGAGACCGGACCTTGAG 240
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Db 181 GCCCATTCAGCTGGCGCTTACTCTGTATTTGGATTTGGACTAGGACGAGACCGGACCTTGAG 240
| | | | |
QY 241 GAGCAATTAACCTTCGGCTCCCGAGAACCGCATTTAGTAAAGGAAAGATGTGCTGTGG 300
| | | | |
Db 241 GAGCAATTAACCTTCGGCTCCCGAGAACCGCATTTAGTAAAGGAAAGATGTGCTGTGG 300
| | | | |
QY 301 TTCCGGCCCACTCTCCTCAATGACACTGCGCACTATACCTGATGTTTAAAGGAACTACTACA 360
| | | | |
Db 301 TTCCGGCCCACTCTCCTCAATGACACTGCGCACTATACCTGATGTTTAAAGGAACTACTACA 360
| | | | |
QY 361 TATTGACAGCAAGTTTGCATTTTCCCTTGGAAAGTTTTCAAAAAGACAGCTGTTTCAATTCC 420
| | | | |
Db 361 TATTGACAGCAAGTTTGCATTTTCCCTTGGAAAGTTTTCAAAAAGACAGCTGTTTCAATTCC 420
| | | | |
QY 421 CCCATGAAATCCCAAGTGCATTAATGATATATAGAAATATGGCAATTCAGAGGATCACTTGT 480
| | | | |
Db 421 CCCATGAAATCCCAAGTGCATTAATGATATATAGAAATATGGCAATTCAGAGGATCACTTGT 480
| | | | |
QY 481 CCAATGTAGATGGATATTTTCCCTTCCAGTGTCAAAACCGACTATCACTTTGGTATATGGGC 540
| | | | |
Db 481 CCAATGTAGATGGATATTTTCCCTTCCAGTGTCAAAACCGACTATCACTTTGGTATATGGGC 540
| | | | |
QY 541 TGTATAAAATACAGAAATTTTAAATATGTAATACCCGAAAGGTATGAACTTTGAGTTTCTCTC 600
| | | | |
Db 541 TGTATAAAATACAGAAATTTTAAATATGTAATACCCGAAAGGTATGAACTTTGAGTTTCTCTC 600
| | | | |
QY 601 ATTGCTTTAAATTTCAAATTAATGAAATTTACATGTGTTTGTATATTCAGAAATGGA 660
| | | | |
Db 601 ATTGCTTTAAATTTCAAATTAATGAAATTTACATGTGTTTGTATATTCAGAAATGGA 660
| | | | |
QY 661 CGTACGTTTCACTCTCACCAGGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAAAATGCA 720
| | | | |
Db 661 CGTACGTTTCACTCTCACCAGGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAAAATGCA 720
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QY 721 GTGCCCCCTGTGATCCATTAATGATCATGTGGTCTATGAGAAAGAACCCAGGAGAG 780
| | | | |
Db 721 GTGCCCCCTGTGATCCATTAATGATCATGTGGTCTATGAGAAAGAACCCAGGAGAG 780
| | | | |
QY 781 GAGTACTCATTCCTGTACGGTCTATTTTAGTGTTCGTGATGATTCGCAATGAGTT 840
| | | | |
Db 781 GAGTACTCATTCCTGTACGGTCTATTTTAGTGTTCGTGATGATTCGCAATGAGTT 840
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QY 841 TGGTGGACCATTTGATGGAAAAAACCCTGATGACATCACTATTGATGTCAACCAATCAAGAA 900
| | | | |
Db 841 TGGTGGACCATTTGATGGAAAAAACCCTGATGACATCACTATTGATGTCAACCAATCAAGAA 900
| | | | |
QY 901 AGTATAAGTCATAGTAGAAACAGAGATGAAACAGAACTCAGATTTTGGAGCATCAAGAAA 960
| | | | |
Db 901 AGTATAAGTCATAGTAGAAACAGAGATGAAACAGAACTCAGATTTTGGAGCATCAAGAAA 960
| | | | |
QY 961 GTTACTCTGAGGATCTCAAGCGCAGCTATGTCTGTCTAGTAGAGTCCCAAGCGGAA 1020
| | | | |
Db 961 GTTACTCTGAGGATCTCAAGCGCAGCTATGTCTGTCTAGTAGAGTCCCAAGCGGAA 1020
| | | | |
QY 1021 GTTGCCAAAGCAGCCAAAGGTGAAGCAGAAAGTGCCAGCTCCCAAGATGCAAGTGA 1080
| | | | |
Db 1021 GTTGCCAAAGCAGCCAAAGGTGAAGCAGAAAGTGCCAGCTCCCAAGATGCAAGTGA 1080
| | | | |
QY 1081 GCTTGTGTTTTGGAGCCACAGTCTGCTAGTG 1113
| | | | |
Db 1081 TGCAAGGAACGTGAAGAAAAATAATTTTAGTG 1113
| | | | |

RESULT 7

US-10-282-162-51
; Sequence 51, Application US/10282162
; Patent No. 6927044
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282,162
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 43
; LENGTH: 2709
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-282-162-51

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; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282,162
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 51
; LENGTH: 2748
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-282-162-51

Query Match      51.8%; Score 1069.6; DB 3; Length 2748;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1072; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ATGACACTTCTGTGGTGTAGTGAAGTCTCTACTTTTATGGAATCCTGCAAGTGATGCC 60
   |||
Db 1 ATGGTGCTTCTGTGGTGTAGTGAAGTCTCTACTTTTATGGAATCCTGCAAGTGATGCC 60

QY 61 TCAGAACGCTGCGATGACTGGGACTAGACACCATGAGGCAAAATCCAAAGTGTGGAAGAT 120
   |||
Db 61 TCAGAACGCTGCGATGACTGGGACTAGACACCATGAGGCAAAATCCAAAGTGTGGAAGAT 120

QY 121 GAGCCAGCTGCGATCAAGTCCCACTCTTTGAACTCTTTGAAATTCAACTACAGCACA 180
   |||
Db 121 GAGCCAGCTGCGATCAAGTCCCACTCTTTGAACTCTTTGAAATTCAACTACAGCACA 180

QY 181 GCCATTACAGCTGGCCCTTACTCTGATCTGTGATTTGGACTAGGACGAGCAGCGACCTTGAG 240
   |||
Db 181 GCCATTACAGCTGGCCCTTACTCTGATCTGTGATTTGGACTAGGACGAGCAGCGACCTTGAG 240

QY 241 GAGCCAAATTAACCTTCGCGCTCCCGAGAACCGCAATAGTAAGGAGAAAGATGTGCTGTGG 300
   |||
Db 241 GAGCCAAATTAACCTTCGCGCTCCCGAGAACCGCAATAGTAAGGAGAAAGATGTGCTGTGG 300

QY 301 TTCGGGCCCACTCTCTCAATGACACTGGCAACTATACCTGCACTGTATGAGAACTACATA 360
   |||
Db 301 TTCGGGCCCACTCTCTCAATGACACTGGCAACTATACCTGCACTGTATGAGAACTACATA 360

QY 361 TATTGAGCAAAAGTTCGATTTCCCTTGGAGTGTGTTCAAAAGACAGCTGTTTCAATTCC 420
   |||
Db 361 TATTGAGCAAAAGTTCGATTTCCCTTGGAGTGTGTTCAAAAGACAGCTGTTTCAATTCC 420

QY 421 CCCATGAAACTCCAGTGCAATAAAGTGTATATAGAAATATGGCAATTCAGAGGATCACTTGT 480
   |||
Db 421 CCCATGAAACTCCAGTGCAATAAAGTGTATATAGAAATATGGCAATTCAGAGGATCACTTGT 480

QY 481 CCAATGTGATGGATATTTTCCCTCCAGTGTCAAAACCGCACTATCACTGGTATATGGGC 540
   |||
Db 481 CCAATGTGATGGATATTTTCCCTCCAGTGTCAAAACCGCACTATCACTGGTATATGGGC 540

QY 541 TGTATAAATACAGAAATTTAATAATGTAATACCCGAAAGGTATGAACTTGATTTCCCTC 600
   |||
Db 541 TGTATAAATACAGAAATTTAATAATGTAATACCCGAAAGGTATGAACTTGATTTCCCTC 600

QY 601 ATTGCCTTAATTTCAAATTAATGAAATTAACATATGTTGTTTACATATCCAGAAATGGA 660
   |||
Db 601 ATTGCCTTAATTTCAAATTAATGAAATTAACATATGTTGTTTACATATCCAGAAATGGA 660

QY 661 CGTACGTTTCATCTCAAGGACTGTGACTGTAAAGGTAGTAGGCTCTCCAAAAATGCA 720
   |||
Db 661 CGTACGTTTCATCTCAAGGACTGTGACTGTAAAGGTAGTAGGCTCTCCAAAAATGCA 720

QY 721 GTGCCCCCTGTGATCCATTCACCTAATGATCATGTGGTCTATGAGAAAGAACAGGAG 780
   |||
Db 721 GTGCCCCCTGTGATCCATTCACCTAATGATCATGTGGTCTATGAGAAAGAACAGGAG 780

QY 781 GAGCTACTCATTTCCCTGTACGGTCTATTTTAGTTTCTCATGATTTCTCGCAATGAGTT 840
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Db 781 GAGCTACTCATTTCCCTGTACGGTCTATTTTAGTTTCTCATGATTTCTCGCAATGAGTT 840
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781 GAGCTACTCATTTCCCTGTACGGTCTATTTTAGTTTCTCATGATTTCTCGCAATGAGTT 840
841 TGGTGGACCATTTGATGGAATAAACTGTATGATGACATCACTATTGATGTCACCAATACGAA 900
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841 TGGTGGACCATTTGATGGAATAAACTGTATGATGACATCACTATTGATGTCACCAATACGAA 900
901 AGTATAAGTCAATAGTAGAAGATGAAACAGAACTCAAGAACTCAGATTTTGAGCATCAAGAA 960
901 AGTATAAGTCAATAGTAGAAGATGAAACAGAACTCAAGAACTCAGATTTTGAGCATCAAGAA 960
961 GTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTCTCATGCTAGAAAGTGCCTCAAGCGCA 1020
961 GTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTCTCATGCTAGAAAGTGCCTCAAGCGCA 1020
1021 GTTGCCAAAGCAGCAGGATGAGGAGCAAGAGTGCCTCAAGTCCCAAGATACACAGTGA 1076
1021 GTTGCCAAAGCAGCAGGATGAGGAGCAAGAGTGCCTCAAGTCCCAAGATACACAGTGA 1076

RESULT 8
US-10-282-162-53
; Sequence 53, Application US/10282162
; Patent No. 6927044
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; TITLE OF INVENTION: AND USING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282,162
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 53
; LENGTH: 2754
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-282-162-53

Query Match      51.8%; Score 1069.6; DB 3; Length 2754;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1072; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ATGACACTTCTGTGGTGTAGTGAAGTCTCTACTTTTATGGAATCCTGCAAGTGATGCC 60
   |||
Db 1 ATGGTGCTTCTGTGGTGTAGTGAAGTCTCTACTTTTATGGAATCCTGCAAGTGATGCC 60

QY 61 TCAGAACGCTGCGATGACTGGGACTAGACACCATGAGGCAAAATCCAAAGTGTGGAAGAT 120
   |||
Db 61 TCAGAACGCTGCGATGACTGGGACTAGACACCATGAGGCAAAATCCAAAGTGTGGAAGAT 120

QY 121 GAGCCAGCTGCGATCAAGTGCCTCTTTGAACTCTTTGAAATTCAACTACAGCACA 180
   |||
Db 121 GAGCCAGCTGCGATCAAGTGCCTCTTTGAACTCTTTGAAATTCAACTACAGCACA 180

QY 181 GCCATTACAGCTGGCCCTTACTCTGATCTGTGATTTGGACTAGGACGAGCAGCGACCTTGAG 240
   |||
Db 181 GCCATTACAGCTGGCCCTTACTCTGATCTGTGATTTGGACTAGGACGAGCAGCGACCTTGAG 240

QY 241 GAGCCAAATTAACCTTCGCGCTCCCGAGAACCGCAATAGTAAGGAGAAAGATGTGCTGTGG 300
   |||
Db 241 GAGCCAAATTAACCTTCGCGCTCCCGAGAACCGCAATAGTAAGGAGAAAGATGTGCTGTGG 300

QY 301 TTCGGGCCCACTCTCTCAATGACACTGGCAACTATACCTGCACTGTATGAGAACTACATA 360
   |||
Db 301 TTCGGGCCCACTCTCTCAATGACACTGGCAACTATACCTGCACTGTATGAGAACTACATA 360

QY 361 TATTGAGCAAAAGTTCGATTTCCCTTGGAGTGTGTTCAAAAGACAGCTGTTTCAATTCC 420
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Db 361 TATTGAGCAAAAGTTCGATTTCCCTTGGAGTGTGTTCAAAAGACAGCTGTTTCAATTCC 420
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Db 675 TGTACTGAAATAGTGACATTTTCATAATGTACTACCGAGGGCATGAACCTTGAGCTTTTC 734
Qy 601 ATTGCCTTAATTTCAATATATGAAATATACATGTTGTTTACATATCCAGAAATGGA 660
Db 735 ATCCCTTGTGTTTCAATATACGGAATATACATGTTGTTTACATATCTGAAACGGA 794
Qy 661 CGTACGTTTCATCTCACAGGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAAATGCA 720
Db 795 CGTCTCTTTTACCTCACAGGACTGTGACTGTAAAGGTGTTGGCTCACCAAGGATGCA 854
Qy 721 GTGCCCCCTGTGATCATCTACCTAATGATCATGTGGTCTATGAGAAAGAACAGAGAG 780
Db 855 TTGCCACCCAGATATTTCTCCAAATGACCGTGTGTTCTATGAGAAAGAACAGAGAG 914
Qy 781 GACTACTACTCCCTGTAGGCTCTATTTAGTTTCTGATGATTTCTCGCATGAGTT 840
Db 915 GAACTGGTTATTCCTTGCAGAGTCTATTTTCAGTTTCATTATGGACTCCCAATGAGTTC 974
Qy 841 TGTGGACCATTTGATGGAAAAAACCTGATGACATCACTATTGATGTCCACCTTACAGAA 900
Db 975 TGTGGACCATTTGATGGAAAAAGCCTGATGAGTCAAGTCAAGTCACTATTATGAA 1034
Qy 901 AGTATAAGTCATAGTAGAAGAGATGAAACAGAACTCAGATTTTGAGCATCAAGAA 960
Db 1035 AGTGTAAATTTCTTCAACGGAAGATGAAACAGGACTCAGATTTTGAGCATCAAGAA 1094
Qy 961 GTTACCTCTGAGATCTCAAGCGCAGCTATGCTGATGCTAGTAGTCCCAAGCGAA 1020
Db 1095 GTACCCCCGAGATCTCAGGCGCAACTATGCTGTCATGCTGCAAAATACCAAGGGAA 1154
Qy 1021 GTTGCCAAAGACGCAAGGTGAAGCAGAAAGTGCAGCTCCAGATACACAGTGAACCTG 1080
Db 1155 GCTGACGAGCTGCCAAGGTGAAGCAGAAAGTACATACCAAGGTACACAGTAGAATC 1214
Qy 1081 GCTGTGGTTTGGAGCCACAGTCCTGCTAGTGGTGAATCTCATTTGTTTACCATGTT 1140
Db 1215 GCCTGTGGTTTGGAGCCACGGTCTTTCTGGTAGTGGTCTCATTTGGTTTACCATGTT 1274
Qy 1141 TACTGGCTAGAGATGCTCTATTTTACCGGCTCATTTTGGACAGATCAAAACCTTTTA 1200
Db 1275 TACTGGCTAGAGATGCTCTTTTACCAGGCTCACTTTGGAAACAGATGAAACATTTCT 1334
Qy 1201 GATGAAAAAGATGATGATATTTATGTATCTTATGCAAGAAATGCGGAAGAAATTT 1260
Db 1335 GATGAAAGAGATGATGATATTTATGTTTCTATGCAAGAAATGCGGAAGAAATTT 1394
Qy 1261 GTATTAAGTACGCTCGTGGAGTTTGGAGAAATGAAATTTGGATACAAAGCTGTGCTTT 1320
Db 1395 GTGCTGCTGACGCTGCGTGGAGTTTGGAGAAATGAGTTTGGATACAAAGCTGTGCTTT 1454
Qy 1321 GACCGAGACGCTGCTCGGGGAAATACAGTGGAGCAGTTTTCATTTTCATTCAGAA 1380
Db 1455 GACAGAGACGCTGCTCGGGGAAATTTGACAGATGAGACCTGAGCTTCATTCAGAA 1514
Qy 1381 AGCAGAGAGATGATTTGTTCTGAGCCTGATGATGACAGAAAGAGCATGAGCATG 1440
Db 1515 AGCAGAGACTCTGTTGTTCTGAGCTTCCAACTAGCTGCTCCAGGGAACACAGCCCTC 1574
Qy 1441 CTGGAGTTTAACTGGGTGTCATGTGCCAGAACTCCATTTG---CCACCAAGCTCATTTG 1497
Db 1575 CTGGAGCTCAAGGCTGGCCCTAGAAAAATATGGCTCCCGGGGCAACATCAACGCTCATTT 1634
Qy 1498 GTTGAATACCGTCCCTTGGACCCCGCAGGAGGATTTCTCAGCTCAAGAGTCTGTG 1557
Db 1635 GTGCAGTACAAAGCTGTGAAGGACATGAAGGTGAAGAGCTGAAGCGGCTAAGACGGTG 1694
Qy 1558 ---TCTTTTGTGAGCTGGAGGAGAGAAAGTCCAAACATTTCTGGCTCTAAATCTTGAA 1614
Db 1695 CTCACGGTCTATTAATGGAAGAGAGAGAAATCCAAGTATCTTCAGGGCAGGTTCTGGAG 1754
Qy 1615 GCTTTCGGTGGCTCTCCCTGA 1639
Db 1755 CAGTTGCGAGTGGCCATGCCAGTGA 1779

RESULT 13
US-10-282-162-33
; Sequence 33, Application US/10282162
; Patent No. 6927044
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; TITLE OF INVENTION: AND USING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282,162
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 1998-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 33
; LENGTH: 2703
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-282-162-33

Query Match 49.3%; Score 1017; DB 3; Length 2703;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 61 TCAGAACGCTGCGATGACTGGGACTAGACACCATGAGGCAATCCAAAGTGTGGAAGAT 120
Db 997 TCAGAACGCTGCGATGACTGGGACTAGACACCATGAGGCAATCCAAAGTGTGGAAGAT 1056
Qy 121 GAGCAGCTCGCATCAAGTGGCCACTCTTTGAACACTTTTGAATTTCAACTACAGCACA 180
Db 1057 GAGCAGCTCGCATCAAGTGGCCACTCTTTGAACACTTTTGAATTTCAACTACAGCACA 1116
Qy 181 GCCAATTACAGCTGGCTTACTCTGATCTGTTATTCGATAGGACGAGCCGGACCTTGAG 240
Db 1117 GCCAATTACAGCTGGCTTACTCTGATCTGTTATTCGATAGGACGAGCCGGACCTTGAG 1176
Qy 241 GAGCAATTAACCTCCGCTCCCGAGAACCGCATTTAGTAAGGAGAAAGATGTGCTGTGG 300
Db 1177 GAGCAATTAACCTCCGCTCCCGAGAACCGCATTTAGTAAGGAGAAAGATGTGCTGTGG 1236
Qy 301 TTCGGGCCACTCTCTCTCAATGACACTGGCAACTATACCTGCAATGTTAAGGAACACTACA 360
Db 1237 TTCGGGCCACTCTCTCTCAATGACACTGGCAACTATACCTGCAATGTTAAGGAACACTACA 1296
Qy 361 TATTGACGCAAAAGTTGCAATTTCCCTTGGAAAGTTGTTCAAAAAGACAGCTGTTTCAATTC 420
Db 1297 TATTGACGCAAAAGTTGCAATTTCCCTTGGAAAGTTGTTCAAAAAGACAGCTGTTTCAATTC 1356
Qy 421 CCCATGAAACTCCCAAGTGCATAAACTGTATATAGAAATATGGCATTTCAGAGGATCACTTGT 480
Db 1357 CCCATGAAACTCCCAAGTGCATAAACTGTATATAGAAATATGGCATTTCAGAGGATCACTTGT 1416
Qy 481 CCAATGTAGATGGATATTTTCTTCCAGTGTCAAAACGACTATCACTTGGTATATGGGC 540
Db 1417 CCAATGTAGATGGATATTTTCTTCCAGTGTCAAAACGACTATCACTTGGTATATGGGC 1476
Qy 541 TGTATATAAATACAGAAATTTTAAATAATGTAATACCCGAGGATGTAACCTTGAGTTTCCCTC 600
Db 1477 TGTATATAAATACAGAAATTTTAAATAATGTAATACCCGAGGATGTAACCTTGAGTTTCCCTC 1536
Qy 601 ATTGCTTTAAATTTCAAATAATGGAATTTACACATGTTGTTTACATATCCAGAAATGGA 660
Db 1537 ATTGCTTTAAATTTCAAATAATGGAATTTACACATGTTGTTTACATATCCAGAAATGGA 1596
Qy 661 CGTAGTTTTCATCTCACAGGACTCTGATGTAAAGGTAGTAGGCTCTCCAAAAAATGCA 720
Db 1597 CGTAGTTTTCATCTCACAGGACTCTGATGTAAAGGTAGTAGGCTCTCCAAAAAATGCA 1656

QY 721 GTGCCCCCTGTGATCCATTCACCTAATGATCATGTGGTCTATGAGAAAGAACCCAGGAG 780
DB 1657 GTGCCCCCTGTGATCCATTCACCTAATGATCATGTGGTCTATGAGAAAGAACCCAGGAG 1716
QY 781 GAGCTACTCATTCCTCTGACGGTCTATTTAGTTTCTGTAGGATTCGCAATGAGTT 840
DB 1717 GAGCTACTCATTCCTCTGACGGTCTATTTAGTTTCTGTAGGATTCGCAATGAGTT 1776
QY 841 TGGTGGACCATTTGATGGAAAAAACCCTGATGACATCACTATTGATGTCCACCATTAACGAA 900
DB 1777 TGGTGGACCATTTGATGGAAAAAACCCTGATGACATCACTATTGATGTCCACCATTAACGAA 1836
QY 901 AGTATAAGTCATPAGTAGAACAGAGATGAAACAGAACTCAGATTTTGGAGCATCAAGAAA 960
DB 1837 AGTATAAGTCATPAGTAGAACAGAGATGAAACAGAACTCAGATTTTGGAGCATCAAGAAA 1896
QY 961 GTTACTCTGAGGATCTCAGCGCAGCTATGTCTGTCTGCTAGAGTGCCTCAAGCGGAA 1020
DB 1897 GTTACTCTGAGGATCTCAGCGCAGCTATGTCTGTCTGCTAGAGTGCCTCAAGCGGAA 1956
QY 1021 GTTGCAAGACGCAAGGTGAAGCAGAAAGTGCAGCTCCCAAGATACACAGTGGAA 1077
DB 1957 GTTGCAAGACGCAAGGTGAAGCAGAAAGTGCAGCTCCCAAGATACACAGTGGAA 2013

RESULT 14

US-10-282-162-35
; Sequence 35, Application US/10282162
; Patent No. 6927044
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282,162
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 35
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-282-162-35

Query Match 49.3%; Score 1017; DB 3; Length 2709;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 61 TCAGAACCTGCGATGACTGGGGACTAGACACCATGAGGCAATCAAGTGTTCAGAT 120
DB 997 TCAGAACCTGCGATGACTGGGGACTAGACACCATGAGGCAATCAAGTGTTCAGAT 1056
QY 121 GAGCCAGCTCGCATCAAGTGGCCACTCTTTGAACACTCTTTGAAATCAACTACAGCACA 180
DB 1057 GAGCCAGCTCGCATCAAGTGGCCACTCTTTGAACACTCTTTGAAATCAACTACAGCACA 1116
QY 181 GCCCATTCAGTGGCCTTACTCTGATCTGTTGTTGATTCGATAGGACGAGCCGGACCTTGA 240
DB 1117 GCCCATTCAGTGGCCTTACTCTGATCTGTTGTTGATTCGATAGGACGAGCCGGACCTTGA 1176
QY 241 GAGCAATTAACCTCCGCTCCCGAGAACCGCATTTAGTAAAGGAAAGATGTGCTGTGG 300
DB 1177 GAGCAATTAACCTCCGCTCCCGAGAACCGCATTTAGTAAAGGAAAGATGTGCTGTGG 1236
QY 301 TTCCGGCCCACTCTCCTCAATGACACTGGCAACTATACCTGATCTTAAGGAACACTACA 360
DB 1237 TTCCGGCCCACTCTCCTCAATGACACTGGCAACTATACCTGATCTTAAGGAACACTACA 1296
QY 361 TATTGACGAAAGTTCATTTCCCTTGGAAAGTTGTTTCAAAAAGACAGCTGTTTCAATTC 420

DB 1297 TATTGACGAAAGTTCATTTCCCTTGGAAAGTTGTTTCAAAAAGACAGCTGTTTCAATTC 1356
QY 421 CCCATGAACCTCCAGTGCATAAAAGTATATAGATATGCAATTCAGAGGATCACTGT 480
DB 1357 CCCATGAACCTCCAGTGCATAAAAGTATATAGATATGCAATTCAGAGGATCACTGT 1416
QY 481 CCAATGTAGATGATATTTTCCCTTCCAGTGTCAAAACCGACTATCACTTGGTATATGGGC 540
DB 1417 CCAATGTAGATGATATTTTCCCTTCCAGTGTCAAAACCGACTATCACTTGGTATATGGGC 1476
QY 541 TGTATATAAATACAGAAATTTTAATAATGTAATACCCGAAAGGTATGAACCTTGAGTTTCCTC 600
DB 1477 TGTATATAAATACAGAAATTTTAATAATGTAATACCCGAAAGGTATGAACCTTGAGTTTCCTC 1536
QY 601 ATTGCCCTTAATTTCAATAATGGAATTTACACATGTGTTGTACATATCCAGAAAATGGA 660
DB 1537 ATTGCCCTTAATTTCAATAATGGAATTTACACATGTGTTGTACATATCCAGAAAATGGA 1596
QY 661 CGTACGTTTCTATCTCACCAGGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAAAATGCA 720
DB 1597 CGTACGTTTCTATCTCACCAGGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAAAATGCA 1656
QY 721 GTGCCCCCTGTGATCCATTCACCTAATGATCATGTGGTCTATGAGAAAGAACCCAGGAG 780
DB 1657 GTGCCCCCTGTGATCCATTCACCTAATGATCATGTGGTCTATGAGAAAGAACCCAGGAG 1716
QY 781 GAGCTACTCATTCCTCTGACGGTCTATTTAGTTTCTGTAGGATTCGCAATGAGTT 840
DB 1717 GAGCTACTCATTCCTCTGACGGTCTATTTAGTTTCTGTAGGATTCGCAATGAGTT 1776
QY 841 TGGTGGACCATTTGATGGAAAAAACCCTGATGACATCACTATTGATGTCCACCATTAACGAA 900
DB 1777 TGGTGGACCATTTGATGGAAAAAACCCTGATGACATCACTATTGATGTCCACCATTAACGAA 1836
QY 901 AGTATAAGTCATPAGTAGAACAGAGATGAAACAGAACTCAGATTTTGGAGCATCAAGAAA 960
DB 1837 AGTATAAGTCATPAGTAGAACAGAGATGAAACAGAACTCAGATTTTGGAGCATCAAGAAA 1896
QY 961 GTTACTCTGAGGATCTCAGCGCAGCTATGTCTGTCTGCTAGAGTGCCTCAAGCGGAA 1020
DB 1897 GTTACTCTGAGGATCTCAGCGCAGCTATGTCTGTCTGCTAGAGTGCCTCAAGCGGAA 1956
QY 1021 GTTGCAAGACGCAAGGTGAAGCAGAAAGTGCAGCTCCCAAGATACACAGTGGAA 1077
DB 1957 GTTGCAAGACGCAAGGTGAAGCAGAAAGTGCAGCTCCCAAGATACACAGTGGAA 2013

RESULT 15

US-10-282-162-37
; Sequence 37, Application US/10282162
; Patent No. 6927044
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282,162
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 37
; LENGTH: 2709
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-282-162-37

Query Match 49.3%; Score 1017; DB 3; Length 2709;
Best Local Similarity 100.0%; Pred. No. 0;

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
OM nucleic - nucleic search, using sw model
Run on: December 14, 2005, 11:12:23 ; Search time 1707 Seconds
(without alignments)
9998.826 Million cell updates/sec

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Perfect score: 2064
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 9793542 seqs, 4134689005 residues
Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
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Listing first 45 summaries

Database : Published Applications NA_Main:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1388.4	67.3	4724	7	US-10-717-597-14
5	1385.2	67.1	1713	5	US-10-215-211-3
6	1075.4	52.1	1077	5	US-10-215-211-5
7	1073	52.0	2703	6	US-10-282-162-39
8	1073	52.0	2703	8	US-10-840-138-9
9	1073	52.0	2703	9	US-10-945-068-9
10	1073	52.0	2703	10	US-11-056-730-9
11	1073	52.0	2703	10	US-11-134-114-39
12	1073	52.0	2709	6	US-10-282-162-41
13	1073	52.0	2709	6	US-10-282-162-43
14	1073	52.0	2709	8	US-10-840-138-11
15	1073	52.0	2709	8	US-10-840-138-13
16	1073	52.0	2709	9	US-10-945-068-11
17	1073	52.0	2709	9	US-10-945-068-13
18	1073	52.0	2709	10	US-11-056-730-11
19	1073	52.0	2709	10	US-11-056-730-13
20	1073	52.0	2709	10	US-11-134-114-41
21	1073	52.0	2709	10	US-11-134-114-43
22	1069.6	51.8	2748	6	US-10-282-162-51
23	1069.6	51.8	2748	8	US-10-840-138-21

24 1069.6 51.8 2748 9 US-10-945-068-21 Sequence 21, Appl
25 1069.6 51.8 2748 10 US-11-056-730-21 Sequence 21, Appl
26 1069.6 51.8 2748 10 US-11-134-114-51 Sequence 51, Appl
27 1069.6 51.8 2754 6 US-10-282-162-53 Sequence 53, Appl
28 1069.6 51.8 2754 8 US-10-840-138-23 Sequence 53, Appl
29 1069.6 51.8 2754 8 US-10-840-138-23 Sequence 23, Appl
30 1069.6 51.8 2754 8 US-10-840-138-25 Sequence 23, Appl
31 1069.6 51.8 2754 9 US-10-945-068-23 Sequence 23, Appl
32 1069.6 51.8 2754 9 US-10-945-068-25 Sequence 25, Appl
33 1069.6 51.8 2754 10 US-11-056-730-23 Sequence 23, Appl
34 1069.6 51.8 2754 10 US-11-056-730-25 Sequence 25, Appl
35 1069.6 51.8 2754 10 US-11-134-114-53 Sequence 53, Appl
36 1069.6 51.8 2754 10 US-11-134-114-55 Sequence 55, Appl
37 1069.2 51.8 2733 3 US-09-313-942-27 Sequence 27, Appl
38 1069.2 51.8 2733 3 US-09-935-868-27 Sequence 27, Appl
39 1069.2 51.8 2733 5 US-10-287-035-27 Sequence 27, Appl
40 1069.2 51.8 2733 6 US-10-282-162-27 Sequence 27, Appl
41 1069.2 51.8 2733 8 US-10-840-138-1 Sequence 1, Appl
42 1069.2 51.8 2733 9 US-10-945-068-1 Sequence 1, Appl
43 1069.2 51.8 2733 10 US-11-056-730-1 Sequence 1, Appl
44 1069.2 51.8 2733 10 US-11-134-114-27 Sequence 27, Appl
45 1067.4 51.7 3355 6 US-10-205-219-24 Sequence 24, Appl

ALIGNMENTS

RESULT 1
US-10-061-727-1
; Sequence 1, Application US/10061727
; Publication No. US20030170632A1
; GENERAL INFORMATION:
; APPLICANT: Sims, John E.
; APPLICANT: Smith, Dirk E.
; TITLE OF INVENTION: IL-1 RECEPTOR ACCESSORY PROTEIN
; FILE REFERENCE: 3151-A
; CURRENT APPLICATION NUMBER: US/10/061,727
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: US 60/244,831
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 2064
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2064)
; OTHER INFORMATION:
; NAME/KEY: misc_feature
; LOCATION: (1792)..(1792)
; OTHER INFORMATION: "n" = a or c. Xaa at amino acid position 598 is Thr or Pro.

Query Match	100.0%;	Score 2063;	DB 6;	Length 2064;
Best Local Similarity	100.0%;	Pred. No. 0;	Mismatches 0;	Indels 0;
Matches 2064;	Conservative	0;		Gaps 0;
QY	1	ATGACACTTCTGTGGTGTAGTGTAGTCTCTACTTTTATGGAATCCTGCAAGTGTATGCC	60	
Db	1	ATGACACTTCTGTGGTGTAGTGTAGTCTCTACTTTTATGGAATCCTGCAAGTGTATGCC	60	
QY	61	TCAGAACCTGCGATGACTGGGGACTAGACACCATGAGGCAATCAAAGTGTGTTGAAGAT	120	
Db	61	TCAGAACCTGCGATGACTGGGGACTAGACACCATGAGGCAATCAAAGTGTGTTGAAGAT	120	
QY	121	GAGCAGCTCCCACTCAAGTCCCACTCTTTGAACTTTTGAATTTCAACTACAGCACA	180	
Db	121	GAGCAGCTCCCACTCAAGTCCCACTCTTTGAACTTTTGAATTTCAACTACAGCACA	180	
QY	181	GCCATTGAGTGGCTTACTCTGATCTGGTATTGACTAGGAGGACCGGACCTTGAG	240	

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Db 181 GCCCATTCAGCTGGCCTTAATCTGATCTGGTATTGGACTAGGACAGGACCGGACCTTGAG 240
Qy 241 GAGCCAAATTAATCTCCGCTCCCGAGAACCGCATTTAGTAAAGGAGAAAGATGTGCTGG 300
Db 241 GAGCCAAATTAATCTCCGCTCCCGAGAACCGCATTTAGTAAAGGAGAAAGATGTGCTGG 300
Qy 301 TTCGGCCCACTCTCCTCAATGACACTGGCAACTATACCTGATGTTAAAGAAACAATA 360
Db 301 TTCGGCCCACTCTCCTCAATGACACTGGCAACTATACCTGATGTTAAAGAAACAATA 360
Qy 361 TATTCAGCAAAAGTTGCAATTTCCCTTGGAAAGTTGTTCAAAAAGACAGCTGTTCAATTCC 420
Db 361 TATTCAGCAAAAGTTGCAATTTCCCTTGGAAAGTTGTTCAAAAAGACAGCTGTTCAATTCC 420
Qy 421 CCCATTGAATCCCAAGTCATATAAATCTGTATATAGAAATATGGCATTCAGAGGATCACTTGT 480
Db 421 CCCATTGAATCCCAAGTCATATAAATCTGTATATAGAAATATGGCATTCAGAGGATCACTTGT 480
Qy 481 CCAAAATGTAGATGGATATTTTCCCTTCCAGTGTCAAACCGACTATCACTTGGTATATGGGC 540
Db 481 CCAAAATGTAGATGGATATTTTCCCTTCCAGTGTCAAACCGACTATCACTTGGTATATGGGC 540
Qy 541 TGTATATAAATACAGAAATTTTAATATGTAATATACCCGAAAGGTATGAACTTGAGTTTCCTC 600
Db 541 TGTATATAAATACAGAAATTTTAATATGTAATATACCCGAAAGGTATGAACTTGAGTTTCCTC 600
Qy 601 ATTGCTTAAATTTCAAATAATGGAATTTACATATGTGTTGTACATATCCAGAAATGGA 660
Db 601 ATTGCTTAAATTTCAAATAATGGAATTTACATATGTGTTGTACATATCCAGAAATGGA 660
Qy 661 CGTACGTTTCATCTCACCAGGACTCTGACTGTAAAGAGTAGTAGGCTCTCCAAAATGCA 720
Db 661 CGTACGTTTCATCTCACCAGGACTCTGACTGTAAAGAGTAGTAGGCTCTCCAAAATGCA 720
Qy 721 GTGCCCCCTGTGATCCATTCACCTAATGATCATGTGGTCTATGAGAAAGAACCCAGGAG 780
Db 721 GTGCCCCCTGTGATCCATTCACCTAATGATCATGTGGTCTATGAGAAAGAACCCAGGAG 780
Qy 781 GAGCTACTCATTCCTGTACGGTCTATTTTAGTTTCTGTGATGTTCTCGCAATGAGGTT 840
Db 781 GAGCTACTCATTCCTGTACGGTCTATTTTAGTTTCTGTGATGTTCTCGCAATGAGGTT 840
Qy 841 TGGTGGACCATGTGAGAAAGAAACCTGATGACATCACTATTGTATGTCAACCATTAACGAA 900
Db 841 TGGTGGACCATGTGAGAAAGAAACCTGATGACATCACTATTGTATGTCAACCATTAACGAA 900
Qy 901 AGTATAAGTCATAGTAGAACAGAGATGAACAAGAACTCAGATTTTGAGCATCAAGAAA 960
Db 901 AGTATAAGTCATAGTAGAACAGAGATGAACAAGAACTCAGATTTTGAGCATCAAGAAA 960
Qy 961 GTTACCTCTGAGGATCTCAAGCGCAGCTATGTCGTGATGTTAGAGTGCCTAAAGGCGAA 1020
Db 961 GTTACCTCTGAGGATCTCAAGCGCAGCTATGTCGTGATGTTAGAGTGCCTAAAGGCGAA 1020
Qy 1021 GTTGCAAGACGACCAAGGTGAAGCAGAAAGTCCAGCTCCAAAGATACACAGTGGAACTG 1080
Db 1021 GTTGCAAGACGACCAAGGTGAAGCAGAAAGTCCAGCTCCAAAGATACACAGTGGAACTG 1080
Qy 1081 GCTGTGGTTTTGGAGCCACAGCTCCTGCTAGTGGTATTCATTTGTTGTTTACCATGTT 1140
Db 1081 GCTGTGGTTTTGGAGCCACAGCTCCTGCTAGTGGTATTCATTTGTTGTTTACCATGTT 1140
Qy 1141 TACTGGCTAGAGATGGTCTATTTTACCGGGCTCATTTTGGAAACAGATGAACCAATTTTA 1200
Db 1141 TACTGGCTAGAGATGGTCTATTTTACCGGGCTCATTTTGGAAACAGATGAACCAATTTTA 1200
Qy 1201 GATGAAAGAGATGATGATATTTATGTATCTTATGCAAGGAATGCGGAAAGAAAGAAATTT 1260
Db 1201 GATGAAAGAGATGATGATATTTATGTATCTTATGCAAGGAATGCGGAAAGAAAGAAATTT 1260
Qy 1261 GTATTACTGACCTCCGTGGAGTTTTGGAGAAATGAAATTTGGATACAAAGCTGTGCATCTTT 1320
Db 1261 GTATTACTGACCTCCGTGGAGTTTTGGAGAAATGAAATTTGGATACAAAGCTGTGCATCTTT 1320
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Qy 1321 GACCGAGACAGTCTGCTGGGGGAAATACAGTGGAAAGCAGTTTTTTGATTTTCATTCAGAGA 1380
Db 1321 GACCGAGACAGTCTGCTGGGGGAAATACAGTGGAAAGCAGTTTTTTGATTTTCATTCAGAGA 1380
Qy 1381 AGCAGAAAGGATGATTTGTTGTTCTGAGCCCTGACTATGTGACAGAAAAGAGCATCAGCATG 1440
Db 1381 AGCAGAAAGGATGATTTGTTGTTCTGAGCCCTGACTATGTGACAGAAAAGAGCATCAGCATG 1440
Qy 1441 CTGAGAGTTAAACTGGGTGTCATGTGCCAGAACTCCATTTGCCACCAAGCTCATTTGTGTT 1500
Db 1441 CTGAGAGTTAAACTGGGTGTCATGTGCCAGAACTCCATTTGCCACCAAGCTCATTTGTGTT 1500
Qy 1501 GAGTACCGTCTCCCTTGAGCACCCGACCCAGCGCATTTCTCAGCTCAAAAGAGTCTGTGTCT 1560
Db 1501 GAGTACCGTCTCCCTTGAGCACCCGACCCAGCGCATTTCTCAGCTCAAAAGAGTCTGTGTCT 1560
Qy 1561 TTTGTGAGCTGGAAGGGAGAAAAGTCCAAACATTTCTGGCTCTAAATTTCTGAAAAGCTTTG 1620
Db 1561 TTTGTGAGCTGGAAGGGAGAAAAGTCCAAACATTTCTGGCTCTAAATTTCTGAAAAGCTTTG 1620
Qy 1621 CGGTTGGCTCTTCCCTGAGAAAGTCTGAGTGCCAGTTCCTGGCTGGAATGAGAGCTGCTCT 1680
Db 1621 CGGTTGGCTCTTCCCTGAGAAAGTCTGAGTGCCAGTTCCTGGCTGGAATGAGAGCTGCTCT 1680
Qy 1681 TCCAGTCTGACATCAGTCTGGATCAGTTTCAAAGGAGGAGAAAGTCTGTTTGAAGAGGCC 1740
Db 1681 TCCAGTCTGACATCAGTCTGGATCAGTTTCAAAGGAGGAGAAAGTCTGTTTGAAGAGGCC 1740
Qy 1741 CCAGAACTTCAGAGCTCAGAGAGGGCTGCAGGTAGCCCTCCAGGCCCAAGGNCNAATGTCC 1800
Db 1741 CCAGAACTTCAGAGCTCAGAGAGGGCTGCAGGTAGCCCTCCAGGCCCAAGGNCNAATGTCC 1800
Qy 1801 AAGCACCAGGAGGAAGTCTCCGCCACCTGCCCTGTTGTGTCACTACTGTGAAGGAGAG 1860
Db 1801 AAGCACCAGGAGGAAGTCTCCGCCACCTGCCCTGTTGTGTCACTACTGTGAAGGAGAG 1860
Qy 1861 AATCACCTTAGGAAACAGAGCGGGCAGAGATTCTAATACAGCCCGCAGTGGGAGACACAC 1920
Db 1861 AATCACCTTAGGAAACAGAGCGGGCAGAGATTCTAATACAGCCCGCAGTGGGAGACACAC 1920
Qy 1921 CTCTGTAAAGCTGTTTCCCAAGAGTCAAGAACTCAATGGATACAAAATGGCACCAGATTG 1980
Db 1921 CTCTGTAAAGCTGTTTCCCAAGAGTCAAGAACTCAATGGATACAAAATGGCACCAGATTG 1980
Qy 1981 GAACCCCTGCTCCCGAGATCTCAGCCCTTGTCTTCATCATTTTACGGACTTATCCCAAT 2040
Db 1981 GAACCCCTGCTCCCGAGATCTCAGCCCTTGTCTTCATCATTTTACGGACTTATCCCAAT 2040
Qy 2041 AACACCGACTTTTATATCCTATAA 2064
Db 2041 AACACCGACTTTTATATCCTATAA 2064
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RESULT 2

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US-10-061-727-3
; Sequence 3, Application US/10061727
; Publication No. US20030170632A1
; GENERAL INFORMATION:
; APPLICANT: Sims, John E.
; APPLICANT: Smith, Dirk E.
; TITLE OF INVENTION: IL-1 RECEPTOR ACCESSORY PROTEIN
; FILE REFERENCE: 3151-A
; CURRENT APPLICATION NUMBER: US/10/061,727
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: US 60/244,831
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 2058
; TYPE: DNA
; ORGANISM: Mus musculus
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RESULT 4
US-10-717-597-14
; Sequence 14, Application US/10717597
; Publication No. US20040110221A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Burczynski, Michael E.
; APPLICANT: Twine, Natalie C.
; APPLICANT: Dorner, Andrew J.
; APPLICANT: Trepicchio, William L.
; APPLICANT: Slonim, Donna K.
; APPLICANT: Stover, Jennifer A.
; TITLE OF INVENTION: METHODS FOR DIAGNOSING RCC AND OTHER SOLID TUMORS
; FILE REFERENCE: AM101080L
; CURRENT APPLICATION NUMBER: US/10/717,597
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US 60/459,782
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: US 60/427,982
; PRIOR FILING DATE: 2002-11-21
; NUMBER OF SEQ ID NOS: 4904
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 4724
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-717-597-14

Query Match 67.3%; Score 1388.4; DB 7; Length 4724;
Best Local Similarity 89.6%; Pred. No. 0;
Matches 1517; Conservative 0; Mismatches 171; Indels 6; Gaps 2;

QY 1 ATGACACTCTGTGGTGTGTAGTGTCTACTTTATGGAATCTCGAAAGTGATGCC 60
DB 207 ATGACACTCTGTGGTGTGTAGTGTCTACTTTATGGAATCTCGAAAGTGATGCC 266

QY 61 TCAGAACGTCGCATCAAGTGGCCACTCTTTGAACTCTTCTGAAATTTCAACTACAGCACA 120
DB 267 TCAGAACGTCGCATCAAGTGGCCACTCTTTGAACTCTTCTGAAATTTCAACTACAGCACA 326

QY 121 GAGCCAGCTCGCATCAAGTGGCCACTCTTTGAACTCTTCTGAAATTTCAACTACAGCACA 180
DB 327 GAGCCAGCTCGCATCAAGTGGCCACTCTTTGAACTCTTCTGAAATTTCAACTACAGCACA 386

QY 181 GCCATTACAGTGGCCCTTACTCTGTATCTGTATTTGAGTGTAGCAGGACCGGACCTTGAG 240
DB 387 GCCATTACAGTGGCCCTTACTCTGTATCTGTATTTGAGTGTAGCAGGACCGGACCTTGAG 446

QY 241 GAGCCAAATTAACCTTCGCGCTCCCGAGAACCGCATTTAGTAAGGAGAAAGATGCTGTGG 300
DB 447 GAGCCAAATTAACCTTCGCGCTCCCGAGAACCGCATTTAGTAAGGAGAAAGATGCTGTGG 506

QY 301 TTCCGGCCCACTCTCCTCAATGACACTGGCAACTATACCTGCAATGTTAAGGAACTACA 360
DB 507 TTCCGGCCCACTCTCCTCAATGACACTGGCAACTATACCTGCAATGTTAAGGAACTACA 566

QY 361 TATTGAGCAAAAGTTGCAATTTCCCTTGGAAAGTTGTTCAAAAAGACAGCTGTTTCAATCC 420
DB 567 TATTGAGCAAAAGTTGCAATTTCCCTTGGAAAGTTGTTCAAAAAGACAGCTGTTTCAATCC 626

QY 421 CCCATGAACCTCCAGTGCATAAAGTGTATATAGAAATATGGCAATTCAGAGGATCACTTGT 480
DB 627 CCCATGAACCTCCAGTGCATAAAGTGTATATAGAAATATGGCAATTCAGAGGATCACTTGT 686

QY 481 CCAATGTAGATGGAATTTTCTTCCAGTGTCAAAACCGCACTATCACTTGTGTATATGGGC 540
DB 687 CCAATGTAGATGGAATTTTCTTCCAGTGTCAAAACCGCACTATCACTTGTGTATATGGGC 746

QY 541 TGTATATAAATACAGAAATTTTAAATATGTAATACCGAAGGTATGAACCTTGATTTTCTC 600
DB 747 TGTATATAAATACAGAAATTTTAAATATGTAATACCGAAGGTATGAACCTTGATTTTCTC 806

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QY 601 ATTGCTTAATTTTCAAATAATGAAATTTACACATGTGTTGTACATATCCAGAAATGGA 660
DB 807 ATTGCTTAATTTTCAAATAATGAAATTTACACATGTGTTGTACATATCCAGAAATGGA 866

QY 661 CGTACGTTTTCATCTCACACAGGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAAATGCA 720
DB 867 CGTACGTTTTCATCTCACACAGGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAAATGCA 926

QY 721 GTGCCCCCTGTGATCCATTCACCTAATGATCATGTGCTCTATGAGAAAGAACACAGAGAG 780
DB 927 GTGCCCCCTGTGATCCATTCACCTAATGATCATGTGCTCTATGAGAAAGAACACAGAGAG 986

QY 781 GAGCTACTCATTTCCCTGTACGGTCTATTTTAGTTTCTCATGATGATTTCTCGCAATGAGTT 840
DB 987 GAGCTACTCATTTCCCTGTACGGTCTATTTTAGTTTCTCATGATGATTTCTCGCAATGAGTT 1046

QY 841 TGGTGGAACCATTTGATGGAAAAAACCCTGATGACATCATCTATTGATGTTCACCAATTAACGAA 900
DB 1047 TGGTGGAACCATTTGATGGAAAAAACCCTGATGACATCATCTATTGATGTTCACCAATTAACGAA 1106

QY 901 AGTATAAGTCATAGTAGAACAAGATGAAACAAGAACTCAGATTTTGTAGCATCAAGAAA 960
DB 1107 AGTATAAGTCATAGTAGAACAAGATGAAACAAGAACTCAGATTTTGTAGCATCAAGAAA 1166

QY 961 GTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTCTAGTGTAGAGTCCCAAGGCGAA 1020
DB 1167 GTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTCTAGTGTAGAGTCCCAAGGCGAA 1226

QY 1021 GTTGCAAGCAGCAAGGTGAAGCAGAAAGTGCAGCTCCCAAGATACACAGTGGAACTG 1080
DB 1227 GTTGCAAGCAGCAAGGTGAAGCAGAAAGTGCAGCTCCCAAGATACACAGTGGAACTG 1286

QY 1081 GCTTGTGTTTGGAGCCACAGTCTCTGTAGTGTGATTTCTCATTTGTTGTTTACCATGTT 1140
DB 1287 GCTTGTGTTTGGAGCCACAGTCTCTGTAGTGTGATTTCTCATTTGTTGTTTACCATGTT 1346

QY 1141 TACTGCTAGAGATGCTCTCTATTTTACCGGCTCATTTTGGAAACAGATCAAAACCATTTTA 1200
DB 1347 TACTGCTAGAGATGCTCTCTATTTTACCGGCTCATTTTGGAAACAGATCAAAACCATTTTA 1406

QY 1201 GATGAAAGAGTATGATATTTATGTATCTTATGCAAGGAATGCGGAAGAAGAATTT 1260
DB 1407 GATGAAAGAGTATGATATTTATGTATCTTATGCAAGGAATGCGGAAGAAGAATTT 1466

QY 1261 GTATTACTGACCTCCGTGGAGTTTGGAGAAATGAAATTTGGATACAAGCTGTGCATCTTT 1320
DB 1467 GTATTACTGACCTCCGTGGAGTTTGGAGAAATGAAATTTGGATACAAGCTGTGCATCTTT 1526

QY 1321 GACCGAGACAGTCTGCTGGGGGAAATACAGTGGAGCAGTCTTTGATTTTCATTCAGACA 1380
DB 1527 GACCGAGACAGTCTGCTGGGGGAAATGTCACAGATGAGACTTTGAGCTTCATTCAGAAA 1586

QY 1381 AGCAGAGGATGATTTGTTCTGAGCCCTGACTATGTGACAGAAAAGAGCATCAAGCATG 1440
DB 1587 AGCAGAGGATGATTTGTTCTGAGCCCTGACTATGTGACAGAAAAGAGCATCAAGCATG 1646

QY 1441 CTGGAGTTTAACTGGGTGTGATGTCAGAACTCAATG---CCACCAAGCTCAATTGTTG 1497
DB 1647 CTGGAGTTTAACTGGGTGTGATGTCAGAAATATGGCTCTCGGGGCAACATCAACGTCATTTTA 1706

QY 1498 GTTGAGTACCGTCCCTTGGACCCCGCACCCAGGCATTTCTCAGCTCAAGAGTCTGTG 1557
DB 1707 GTTGAGTACCGTCCCTTGGACCCCGCACCCAGGCATTTCTCAGCTCAAGAGTCTGTG 1766

QY 1558 ---TCTTTTGTGAGCTGGAAGGGAGAAAAGTCCAAACATTTCTGGCTCTAAATTTCTGGAAA 1614
DB 1767 CTCAGGTCATTAATGGAAGGGGAAAATCCAAAGTATCCACAGGCGAGTTCTTGGAAAG 1826

QY 1615 GCTTTGCGGTTGGCTCTTCCCTGTGAAAGTCTGAGTGCAGTCTTGGCTGGAAGTCAAGAGC 1674
DB 1827 GAGCTGCGGTTGGCTCTTCCCTGTGAAAGTCTGAGTGCAGTCTTGGCTGGAAGTCAAGAGC 1886

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QY 1675 TGCTCTTCCAGTC 1688
Db 1887 GGCCTCTCGTATTC 1900

RESULT 5
US-10-215-211-3
; Sequence 3, Application US/10215211
; Publication No. US20030049255A1
; GENERAL INFORMATION:
; APPLICANT: Sims, John E.
; APPLICANT: Smith, Dirk E.
; TITLE OF INVENTION: INTERLEUKIN-1 RECEPTORS IN THE TREATMENT OF DISEASES
; FILE REFERENCE: 3321-A
; CURRENT APPLICATION NUMBER: US/10/215,211
; CURRENT FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: US 60/310,789
; PRIOR FILING DATE: 2001-08-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1713
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1713)
; OTHER INFORMATION:
US-10-215-211-3

Query Match 67.1%; Score 1385.2; DB 5; Length 1713;
Best Local Similarity 89.4%; Pred. No. 0;
Matches 1515; Conservative 0; Mismatches 173; Indels 6; Gaps 2;

QY 1 ATGACACTCTCTGGTGTAGTGTAGTCTCTACTTTTATGGAATCCTGCAAGTATGCC 60
Db 1 ATGACACTCTCTGGTGTAGTGTAGTGTAGTCTCTACTTTTATGGAATCCTGCAAGTATGCC 60

QY 61 TCAGAACCGTGGGATGACTGGGGACTAGACACCATGAGGCAATCCAAAGTGTTCAGAT 120
Db 61 TCAGAACCGTGGGATGACTGGGGACTAGACACCATGAGGCAATCCAAAGTGTTCAGAT 120

QY 121 GAGCAGCTCGCATCAAGTGGCCACTCTTTTGAACACTTCTTGAAATCAACTACAGACA 180
Db 121 GAGCAGCTCGCATCAAGTGGCCACTCTTTTGAACACTTCTTGAAATCAACTACAGACA 180

QY 181 GCCCATTCAGCTGGCCTTACTCTGATCTGGTATTGGACTAGCAGGACGGGACCTTGAG 240
Db 181 GCCCATTCAGCTGGCCTTACTCTGATCTGGTATTGGACTAGCAGGACGGGACCTTGAG 240

QY 241 GAGCCAAATTAATTCGGCTCCCGAGAACCGCATTTAGTAAGGAGAAAGATGTGCTGTGG 300
Db 241 GAGCCAAATTAATTCGGCTCCCGAGAACCGCATTTAGTAAGGAGAAAGATGTGCTGTGG 300

QY 301 TTCGGGCCACTCTCTCAATGACACTGGCAACTATACCTGATGTTAAGGAACACTACA 360
Db 301 TTCGGGCCACTCTCTCAATGACACTGGCAACTATACCTGATGTTAAGGAACACTACA 360

QY 361 TATTCAGCAAGTGTGCATTTCCCTTGGAGTGTTCAAAAGACAGCTGTTCAATTC 420
Db 361 TATTCAGCAAGTGTGCATTTCCCTTGGAGTGTTCAAAAGACAGCTGTTCAATTC 420

QY 421 CCCATGAACCTCCAGTGCATAAACTGTATATAGAAATATGGCAATTCAGAGGATCACTTGT 480
Db 421 CCCATGAACCTCCAGTGCATAAACTGTATATAGAAATATGGCAATTCAGAGGATCACTTGT 480

QY 481 CCAATGTAGATGGATATTTTCCTTCCAGTGTCAAAACCGACTATCACTTTGATATGGGC 540
Db 481 CCAATGTAGATGGATATTTTCCTTCCAGTGTCAAAACCGACTATCACTTTGATATGGGC 540

QY 541 TGTATATAAATACAGAAATTTTAAATATGTAATACCCGAGGATGAACTTGAGTTTCCTC 600
Db 541 TGTATATAAATACAGAAATTTTAAATATGTAATACCCGAGGATGAACTTGAGTTTCCTC 600

1601 ATTGCTTTAAATTTCAAATAATGGAATTTACACATGTGTGTTTACATATCCAGAAAATGGA 660
1601 ATTGCTTTAAATTTCAAATAATGGAATTTACACATGTGTGTTTACATATCCAGAAAATGGA 660
1661 CGTACGTTTTCATCTCACAGGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAAAATGCA 720
1661 CGTACGTTTTCATCTCACAGGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAAAATGCA 720
1721 GTGCCCCCTGTGATCCATTACCTTAATGATCATGTGGTCTATGAGAAAGAACCCAGGAG 780
1721 GTGCCCCCTGTGATCCATTACCTTAATGATCATGTGGTCTATGAGAAAGAACCCAGGAG 780
1781 GAGTACTCTCATTCCTGTACCGTCTATTTTATGTTTCTGATGGATTTCTGCAATGAGGTT 840
1781 GAGTACTCTCATTCCTGTACCGTCTATTTTATGTTTCTGATGGATTTCTGCAATGAGGTT 840
1841 TGGTGGACCATGTGATGGAAAAAACCTGATGACATCACTATTTGATGTCACTTAAACGAA 900
1841 TGGTGGACCATGTGATGGAAAAAACCTGATGACATCACTATTTGATGTCACTTAAACGAA 900
1901 AGTATAAGTCATAGTAGAACAGATGAAACAGAACTCAGATTTTTCAGCATCAAGAA 960
1901 AGTATAAGTCATAGTAGAACAGATGAAACAGAACTCAGATTTTTCAGCATCAAGAA 960
1961 GTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTCTATGCTAGAAAGTCCAAAGCGAA 1020
1961 GTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTCTATGCTAGAAAGTCCAAAGCGAA 1020
1021 GTTCCAAAGCAGCAAGGTGAAGAGAAAGTCCAGCTCCAAAGATACACAGTGGAACTG 1080
1021 GTTCCAAAGCAGCAAGGTGAAGAGAAAGTCCAGCTCCAAAGATACACAGTGGAACTG 1080
1081 GCTTGTGGTGTGGAGCCACAGTCTCTGCTAGTGTGATTTCTCATTTGTTTACCATGTT 1140
1081 GCTTGTGGTGTGGAGCCACAGTCTCTGCTAGTGTGATTTCTCATTTGTTTACCATGTT 1140
1141 TACTGGCTAGAGATGGTCTTATTTTACCGGGCTCATTTTGGAAACAGATGAAACCATTTTA 1200
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1201 GATGGAAGAAGATATGATATTTATGATCTCTATGCAAGAAATGCGGAAGAAAGAAATTT 1260
1201 GATGGAAGAAGATATGATATTTATGATCTCTATGCAAGAAATGCGGAAGAAAGAAATTT 1260
1261 GTATTACTGACCTCCGTTGGAGATTTGGAGAAATGAAATTTGGATACAGCTGTGCATCTTT 1320
1261 GTTTTACTGACCTCCGTTGGAGATTTGGAGAAATGAAATTTGGATACAGCTGTGCATCTTT 1320
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1321 GACCGAGACAGTCTGCTGGGGGAAATTTGTACAGATGAGACTTTTGAGCTTCATTCAGAAA 1380
1381 AGCAGAAGGATGATGTTGTTCTGAGCCTGACTATGTGACAGAAAGAGCATCAGCATG 1440
1381 AGCAGAAGGATGATGATGTTGTTCTGAGCCTGACTATGTGACAGAAAGAGCATCAGCATG 1440
1441 CTGAGGTTTAAACTGGGTGTCATGTCGCAGAACTCCATTG--CCACCAAGCTCAATCTGTG 1497
1441 CTGAGGTTTAAACTGGGTGTCATGTCGCAGAACTCCATTG--CCACCAAGCTCAATCTGTG 1497
1498 GTTGAGTACCGTCCCTTTGAGCACCAGCAGCTTCTTCAAGTCTTCAAGTCAAGAGAGTCTGTG 1557
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1501 GTACAGTACAAAGCTGTGAGGAAACGAAAGGTGAAGAGCTGAAGAGGGCTTAAGACGGTG 1560
1501 GTACAGTACAAAGCTGTGAGGAAACGAAAGGTGAAGAGCTGAAGAGGGCTTAAGACGGTG 1560
1558 ---TCTTTTGTGAGCTGGAAGGAGAAAGTCCAAACATTTCTGGCTCTAAATTTCTGGAAA 1614
1558 ---TCTTTTGTGAGCTGGAAGGAGAAAGTCCAAACATTTCTGGCTCTAAATTTCTGGAAA 1614
1561 CTCAGGTCATTAATGGAAGGGGAAATCCAAAGTATCCACAGGGCAGGTTCTGGAAG 1620
1561 CTCAGGTCATTAATGGAAGGGGAAATCCAAAGTATCCACAGGGCAGGTTCTGGAAG 1620
1615 GCTTTGGGTTGGGCTCTTCCCTCGAAGTCTGAGTGCAGTCTTGGCTGGAATGAGAGC 1674
1615 GCTTTGGGTTGGGCTCTTCCCTCGAAGTCTGAGTGCAGTCTTGGCTGGAATGAGAGC 1674
1621 CAGTGCAGGTGGCCATGCCAGTGAAGAAAGTCCAGGCGGTCTAGCAGTGTAGGAGCAG 1680
1621 CAGTGCAGGTGGCCATGCCAGTGAAGAAAGTCCAGGCGGTCTAGCAGTGTAGGAGCAG 1680
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Qy 1675 TGCTCTTCCCAGTC 1688
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Db 1681 GGCTCTCGTATTC 1694

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RESULT 6
US-10-215-211-5
; Sequence 5, Application US/10215211
; Publication No. US20030049255A1
; GENERAL INFORMATION:
; APPLICANT: Sims, John E.
; APPLICANT: Smith, Dirk E.
; TITLE OF INVENTION: INTERLEUKIN-1 RECEPTORS IN THE TREATMENT OF DISEASES
; FILE REFERENCE: 3321-A
; CURRENT APPLICATION NUMBER: US/10/215,211
; PRIOR FILING DATE: 2002-08-07
; CURRENT APPLICATION NUMBER: US 60/310,789
; PRIOR FILING DATE: 2001-08-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 1077
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1077)
; OTHER INFORMATION:
US-10-215-211-5

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QY	601	ATTGCCCTTAATTTCAAATAATGGAAATTTACACATGTGTGTTTACATATCCAGAAAATGGAA	660
DB	601	ATTGCCCTTAATTTCAAATAATGGAAATTTACACATGTGTGTTTACATATCCAGAAAATGGAA	660
QY	661	CGTAGCTTTTCATCTCACACAGGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAAAATGGCA	720
DB	661	CGTAGCTTTTCATCTCACACAGGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAAAATGGCA	720
QY	721	GTGCCCCCTGTGATCCATTCACTTAATGATCATCTGTGCTATGAGAAAGAACCCAGGAGAG	780
DB	721	GTGCCCCCTGTGATCCATTCACTTAATGATCATCTGTGCTATGAGAAAGAACCCAGGAGAG	780
QY	781	GAGCTACTCATTTCCCTGTACGGTCTATTTTAGTTTCTGTGATGGATTCTCCCAATGAGGTT	840
DB	781	GAGCTACTCATTTCCCTGTACGGTCTATTTTAGTTTCTGTGATGGATTCTCCCAATGAGGTT	840
QY	841	TGTTGGACCATTTGATGGAAAAAAACCTGTATGACATCACTATTGATGTCAACCATTAACGAA	900
DB	841	TGTTGGACCATTTGATGGAAAAAAACCTGTATGACATCACTATTGATGTCAACCATTAACGAA	900
QY	901	AGTATAGTCTATGATAGNACAGAGATGAAACAGAACTCAGATTTTGGAGCATCAAGAA	960
DB	901	AGTATAGTCTATGATAGNACAGAGATGAAACAGAACTCAGATTTTGGAGCATCAAGAA	960
QY	961	GTTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTCTAGTAAGTGCCTCAAGGCGGAA	1020
DB	961	GTTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTCTAGTAAGTGCCTCAAGGCGGAA	1020
QY	1021	GTTGCCAAAGCAGCCAAAGGTGAAGCAGAAAGTGCAGCTCCAAGATACACAGTGGAA	1077
DB	1021	GTTGCCAAAGCAGCCAAAGGTGAAGCAGAAAGTGCAGCTCCAAGATACACAGTGGAA	1077

[illegible]

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RESULT 7
US-10-282-162-39
; Sequence 39, Application US/10282162
; Publication No. US20030143697A1
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; TITLE OF INVENTION: AND USING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282,162
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 39
; LENGTH: 2703
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-282-162-39

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Db 841 TGGTGGACCAATTGATGAAAAAACCTGATGACATCACTATTGATGTCACCAATTAACGAA 900
Qy 901 AGTATAAGTCTAGTAGAACAGAAAGATGAACAAAGAACTCAGATTTTGGAGCATCAAGAAA 960
Db 901 AGTATAAGTCTAGTAGAACAGAAAGATGAACAAAGAACTCAGATTTTGGAGCATCAAGAAA 960
Qy 961 GTTACCTCTGAGGATCTCAAGCGAGCTATGCTGTCATGCTAGCAAGTGCACCAAGGCGAA 1020
Db 961 GTTACCTCTGAGGATCTCAAGCGAGCTATGCTGTCATGCTAGCAAGTGCACCAAGGCGAA 1020
Qy 1021 GTTGCCAAAGCAGCAAGGTTGAAGCAGAAAGTGCAGCTCCAGATACACAGATGGAAGTGC 1080
Db 1021 GTTGCCAAAGCAGCAAGGTTGAAGCAGAAAGTGCAGCTCCAGATACACAGATGGAAGTGC 1080
Qy 1081 CTTTGTGGTTTGGAGCCACAGTCTCTGCTAGTG 1113
Db 1081 TGAAGGAACGTGAAGAAAAAATAATTTTAGTG 1113

RESULT 9
US-10-945-068-9
; Sequence 9, Application US/10945068
; Publication No. US20050129685A1
; GENERAL INFORMATION:
; APPLICANT: Jingtai Cao
; TITLE OF INVENTION: USE OF IL-1 BLOCKERS TO PREVENT CORNEAL INFLAMMATION
; FILE REFERENCE: REG 2084
; CURRENT APPLICATION NUMBER: US/10/945,068
; PRIOR FILING DATE: 2004-09-20
; PRIOR APPLICATION NUMBER: 60/503,854
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 2703
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-945-068-9

Query Match 52.0%; Score 1073; DB 9; Length 2703;
Best Local Similarity 97.8%; Pred. No. 0;
Matches 1088; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

Qy 1 ATGACACTCTGTGGTGTAGTGAGTCTCTACTTTTATGGAATCTCTGCAAAAGTGATGCC 60
Db 1 ATGGTGTCTTCTGTGGTGTAGTGAGTCTCTACTTTTATGGAATCTCTGCAAAAGTGATGCC 60

Qy 61 TCAGAACGCTGCGATGACTGGGACTAGACACCATGAGGCAATCCAGTGTGTAAGAT 120
Db 61 TCAGAACGCTGCGATGACTGGGACTAGACACCATGAGGCAATCCAGTGTGTAAGAT 120

Qy 121 GAGCCAGCTCGCATCAAGTCCCACTCTTTGAACACTCTTTGAATTTCAACTACAGACA 180
Db 121 GAGCCAGCTCGCATCAAGTCCCACTCTTTGAACACTCTTTGAATTTCAACTACAGACA 180

Qy 181 GCCATTACGCTGGCCTTACTCTGATCTGATATGGAATAGGAGGACCGGACCTTGAG 240
Db 181 GCCATTACGCTGGCCTTACTCTGATCTGATATGGAATAGGAGGACCGGACCTTGAG 240

Qy 241 GAGCCAAATTAATCTCCGCTCCCGAGAACCGCATAGTAAGAGAAAGATGCTGTGG 300
Db 241 GAGCCAAATTAATCTCCGCTCCCGAGAACCGCATAGTAAGAGAAAGATGCTGTGG 300

Qy 301 TTCGGGCCACTCTCTCAATGACACTGGCAACTATACCTGCAATGTTAAGGAACACTACA 360
Db 301 TTCGGGCCACTCTCTCAATGACACTGGCAACTATACCTGCAATGTTAAGGAACACTACA 360

Qy 361 TATTGCAAGCAAGTGTCAATTCCTTGGAAAGTTGTTCAAAAAGACAGCTGTTTCAATTC 420
Db 361 TATTGCAAGCAAGTGTCAATTCCTTGGAAAGTTGTTCAAAAAGACAGCTGTTTCAATTC 420
```

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Qy 421 CCCATGAAACTCCAGTGCATAAACTGTATATAGAAATATGGCATTCCAGAGGATCACTTGT 480
Db 421 CCCATGAAACTCCAGTGCATAAACTGTATATAGAAATATGGCATTCCAGAGGATCACTTGT 480
Qy 481 CCAAAATGTAGATGGATATTTTCTTCCAGTGTCAAAACCGCATATCACTTGGTATATGGGC 540
Db 481 CCAAAATGTAGATGGATATTTTCTTCCAGTGTCAAAACCGCATATCACTTGGTATATGGGC 540
Qy 541 TGTATATAAATACAGAAATTTTAAATGTAATACCCGAAGGTATGAACCTTGAGTTTCTTC 600
Db 541 TGTATATAAATACAGAAATTTTAAATGTAATACCCGAAGGTATGAACCTTGAGTTTCTTC 600
Qy 601 ATTGCCTTAATTTCAAAATTAATGGAATTAACATGTTGTTTACATATCCAGAAATGGA 660
Db 601 ATTGCCTTAATTTCAAAATTAATGGAATTAACATGTTGTTTACATATCCAGAAATGGA 660
Qy 661 CGTACGTTTCACTCTCAACAGGACTCTGACTGTAAGGTAGTAGGCTCTCCAAAAATGCA 720
Db 661 CGTACGTTTCACTCTCAACAGGACTCTGACTGTAAGGTAGTAGGCTCTCCAAAAATGCA 720
Qy 721 GTGCCCCCTGTGATCCATTCACTAATGATCATGTGGTCTATGAGAAAGAACCCAGAGAG 780
Db 721 GTGCCCCCTGTGATCCATTCACTAATGATCATGTGGTCTATGAGAAAGAACCCAGAGAG 780
Qy 781 GAGCTACTCATTTCCCTGTAGGCTCTATTTTAGTTTCTGATGGATTTCTCGCAATGAGTT 840
Db 781 GAGCTACTCATTTCCCTGTAGGCTCTATTTTAGTTTCTGATGGATTTCTCGCAATGAGTT 840
Qy 841 TGTGGACCAATTGATGAAAAAAACCTGATGATCATCACTATTGATGTCAACATTAAACGAA 900
Db 841 TGTGGACCAATTGATGAAAAAAACCTGATGATCATCACTATTGATGTCAACATTAAACGAA 900
Qy 901 AGTATAAGTCTAGTAGTAAGACAGAAAGATGAACAAAGAACTCAGATTTTGAAGATCAAGAA 960
Db 901 AGTATAAGTCTAGTAGTAAGACAGAAAGATGAACAAAGAACTCAGATTTTGAAGATCAAGAA 960
Qy 961 GTTACCTCTGAGGATCTCAAGCGAGCTATGCTGTCATGCTAGTAGAGTGCCTAAGGCGAA 1020
Db 961 GTTACCTCTGAGGATCTCAAGCGAGCTATGCTGTCATGCTAGTAGAGTGCCTAAGGCGAA 1020
Qy 1021 GTTGCCAAAGCAGCAAGGTTGAAGCAGAAAGTGCAGCTCCAGATACACAGATGGAAGTGC 1080
Db 1021 GTTGCCAAAGCAGCAAGGTTGAAGCAGAAAGTGCAGCTCCAGATACACAGATGGAAGTGC 1080
Qy 1081 GCTTGTGGTTTGGAGCCACAGTCTCTGCTAGTG 1113
Db 1081 TGAAGGAACGTGAAGAAAAAATAATTTTAGTG 1113

RESULT 10
US-11-056-730-9
; Sequence 9, Application US/11056730
; Publication No. US20050197293A1
; GENERAL INFORMATION:
; APPLICANT: Mellis, Scott
; APPLICANT: Stahl, Neil
; APPLICANT: Radin, Allen
; APPLICANT: Weinstein, Steven
; APPLICANT: Calaprice, Denise
; APPLICANT: Karow, Margaret
; APPLICANT: Papadopoulos, Joanne
; TITLE OF INVENTION: Use of an IL-1 Antagonist for Treating Arthritis
; FILE REFERENCE: 203G
; CURRENT APPLICATION NUMBER: US/11/056,730
; CURRENT FILING DATE: 2005-02-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 2703
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
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Db 421 CCCATGAACTCCAGTGATATAAATCTGATATAGAAATATGGCAATCAGAGATCACCTGT 480
Qy 481 CCAATGTAGATGATATTTTCCCTCCAGTGTCAAACCGGACTATACCTTGGTATATGGC 540
Db 481 CCAATGTAGATGATATTTTCCCTCCAGTGTCAAACCGGACTATACCTTGGTATATGGC 540
Qy 541 TGTATATAATACAGAAATTTTAAATATGTAATACCCGAAGGTATGAACCTTGAGTTTCCTC 600
Db 541 TGTATATAATACAGAAATTTTAAATATGTAATACCCGAAGGTATGAACCTTGAGTTTCCTC 600
Qy 601 ATTGCCCTTAATTCCAAATAATGGAATTTACACATGTGTGTTGTTACATATCCAGAAAAATGGA 660
Db 601 ATTGCCCTTAATTCCAAATAATGGAATTTACACATGTGTGTTGTTACATATCCAGAAAAATGGA 660
Qy 661 CGTACGTTTATCTCACAGGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAAAATGCA 720
Db 661 CGTACGTTTATCTCACAGGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAAAATGCA 720
Qy 721 GTGCCCCCTGTGATCCCAATTCACCTTAATGATCATGTGTCTATGAGAAAGAACAGAGAG 780
Db 721 GTGCCCCCTGTGATCCCAATTCACCTTAATGATCATGTGTCTATGAGAAAGAACAGAGAG 780
Qy 781 GAGCTACTCATTCCTGTACGGTCTATTTTAGTGTCTGATGGATTCTCGCAATGAGGTT 840
Db 781 GAGCTACTCATTCCTGTACGGTCTATTTTAGTGTCTGATGGATTCTCGCAATGAGGTT 840
Qy 841 TGTGGACCAATGTAGAAAAAACCTGATGACATCACTATTGATGTCACCATTAACGAA 900
Db 841 TGTGGACCAATGTAGAAAAAACCTGATGACATCACTATTGATGTCACCATTAACGAA 900
Qy 901 AGTATAAGTCATAGTAGAACAGAGATGAAACAGAACTCAGATTTTGGACCAAGAAA 960
Db 901 AGTATAAGTCATAGTAGAACAGAGATGAAACAGAACTCAGATTTTGGACCAAGAAA 960
Qy 961 GTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTATGATGAGAGTGCACCAAGGCGAA 1020
Db 961 GTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTATGATGAGAGTGCACCAAGGCGAA 1020
Qy 1021 GTTGCCAAAGCAGCGCAAGGTGAAGCAAAAGTGCAGCTCCAAAGATACACAGTGGAAAA 1080
Db 1021 GTTGCCAAAGCAGCGCAAGGTGAAGCAAAAGTGCAGCTCCAAAGATACACAGTGGAAAA 1080
Qy 1081 GCTTGTGGTTTGGAGCCACAGTCTCTAGTG 1113
Db 1081 TGCAGGAACGTGAAGAAAAATAATTTTAGTG 1113

RESULT 12
US-10-282-162-41
; Sequence 41. Application US/10282162
; Publication No. US20030143697A1
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282,162
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 41
; LENGTH: 2709
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-282-162-41

Query Match 52.0%; Score 1073; DB 6; Length 2709;
Best Local Similarity 97.8%; Pred. No. 0;

Matches 1088; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
Qy 1 ATGACACTTCTGTGGTGTGTAGTACTCTACTTTTATGGAATCTCTGCAAGATGATGCC 60
Db 1 ATGGTCTTCTGTGGTGTGTAGTACTCTACTTTTATGGAATCTCTGCAAGATGATGCC 60
Qy 61 TCAGAAAGCGTGCATGACTGGGGACTAGACACCATGAGGCAAAATCCAAAGTGTGTTGAAGAT 120
Db 61 TCAGAAAGCGTGCATGACTGGGGACTAGACACCATGAGGCAAAATCCAAAGTGTGTTGAAGAT 120
Qy 121 GAGCCAGCTGCGATCAAGTGGCCCACTCTTTTGAACACATCTTTGAAATTTCAACTACAGCACA 180
Db 121 GAGCCAGCTGCGATCAAGTGGCCCACTCTTTTGAACACATCTTTGAAATTTCAACTACAGCACA 180
Qy 181 GCCCATTTCACTGGCCCTTACTCTGATCTGTTTGGACTAGGACGAGACCGGACCTTGAG 240
Db 181 GCCCATTTCACTGGCCCTTACTCTGATCTGTTTGGACTAGGACGAGACCGGACCTTGAG 240
Qy 241 GAGCCAAATTAACCTTCCGCCCTCCCGAGAACCGCATTTAGTAAAGGAGAAAGATGTCGTGG 300
Db 241 GAGCCAAATTAACCTTCCGCCCTCCCGAGAACCGCATTTAGTAAAGGAGAAAGATGTCGTGG 300
Qy 301 TTCGGGCCCACTCTCTCAATGACACTGGCAACTATACCTGTCATGTTTAAAGAAACACTACA 360
Db 301 TTCGGGCCCACTCTCTCAATGACACTGGCAACTATACCTGTCATGTTTAAAGAAACACTACA 360
Qy 361 TATTGACAGAAAGTTCGATTTCCCTTTGGAAGTTGTTTCAAAAGACAGCTGTTTCAATTC 420
Db 361 TATTGACAGAAAGTTCGATTTCCCTTTGGAAGTTGTTTCAAAAGACAGCTGTTTCAATTC 420
Qy 421 CCCATGAACTCCAGTGCATAACTGTATATAGAAATATGGCAATTCAGAGGATCACCTGT 480
Db 421 CCCATGAACTCCAGTGCATAACTGTATATAGAAATATGGCAATTCAGAGGATCACCTGT 480
Qy 481 CCAAAATGTAGATGGAATTTTCCCTTCCAGTGTCAAAACCGACTATCACTTGGTATATGGGC 540
Db 481 CCAAAATGTAGATGGAATTTTCCCTTCCAGTGTCAAAACCGACTATCACTTGGTATATGGGC 540
Qy 541 TGTATATAATACAGAAATTTTAAATATGTAATACCCGAAGGTATGAACCTTGAGTTTCCTC 600
Db 541 TGTATATAATACAGAAATTTTAAATATGTAATACCCGAAGGTATGAACCTTGAGTTTCCTC 600
Qy 601 ATTGCCCTTAATTCCAAATAATGGAATTTACACATGTGTGTTTATGATGATTTCTGCAATGAGGTT 840
Db 601 ATTGCCCTTAATTCCAAATAATGGAATTTACACATGTGTGTTTATGATGATTTCTGCAATGAGGTT 840
Qy 841 TGTGGACCAATGTAGAAAAAACCTGATGACATCACTATTGATGTCACCATTAACGAA 900
Db 841 TGTGGACCAATGTAGAAAAAACCTGATGACATCACTATTGATGTCACCATTAACGAA 900
Qy 901 AGTATAAGTCATAGTAGAACAGAGATGAAACAGAACTCAGATTTTGGACCAAGAAA 960
Db 901 AGTATAAGTCATAGTAGAACAGAGATGAAACAGAACTCAGATTTTGGACCAAGAAA 960
Qy 961 GTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTCTAGTAAAGTGCACCAAGGCGAA 1020
Db 961 GTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTCTAGTAAAGTGCACCAAGGCGAA 1020
Qy 1021 GTTGCCAAAGCAGCGCAAGGTGAAGCAAAAGTGCAGCTCCAAAGATACACAGTGGAACTG 1080
Db 1021 GTTGCCAAAGCAGCGCAAGGTGAAGCAAAAGTGCAGCTCCAAAGATACACAGTGGAA 1080

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QY 1081 GCTTGTGGTTTTGGAGCCACAGCTCCTGCTAGTG 1113
Db 1081 TGCAAGGAACGTGAAGAAAAATAATTTTAGTG 1113

RESULT 13
US-10-282-162-43
; Sequence 43, Application US/10282162
; Publication No. US20030143697A1
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282,162
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 43
; LENGTH: 2709
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-282-162-43

Query Match 52.0%; Score 1073; DB 6; Length 2709;
Best Local Similarity 97.8%; Pred. No. 0;
Matches 1088; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 1 ATGACACTCTGTGGTGTGTAGTGAGTCTCTACTTTTATGGATCCTGCAAGTGTATGCC 60
Db 1 ATGGTCTCTGTGGTGTGTAGTGAGTCTCTACTTTTATGGATCCTGCAAGTGTATGCC 60

QY 61 TCAGAACGCTGCGATGACCTGGGACCTAGACACCATGAGGCAATCCAAAGTGTGAAGAT 120
Db 61 TCAGAACGCTGCGATGACCTGGGACCTAGACACCATGAGGCAATCCAAAGTGTGAAGAT 120

QY 121 GAGCCAGCTCGCATCAAGTGGCCACCTCTTTGAACTCTTTGAACTCTTTGAACTCAAGTACAGCACA 180
Db 121 GAGCCAGCTCGCATCAAGTGGCCACCTCTTTGAACTCTTTGAACTCAAGTACAGCACA 180

QY 181 GCCATTTCAGCTGGCCCTTACTCTGATCTGTATTTGACTAGGACGAGCCGACCTTGAG 240
Db 181 GCCATTTCAGCTGGCCCTTACTCTGATCTGTATTTGACTAGGACGAGCCGACCTTGAG 240

QY 241 GAGCCAAATTAACCTTCGCGCTCCCGAGAACCGCATTTAGTAAAGAGAAAGATGTGCTGTGG 300
Db 241 GAGCCAAATTAACCTTCGCGCTCCCGAGAACCGCATTTAGTAAAGAGAAAGATGTGCTGTGG 300

QY 301 TTCGCGCCCACTCTCTCAATGACACTGGCAACTATACCTGATGTTAAGGAACACTACA 360
Db 301 TTCGCGCCCACTCTCTCAATGACACTGGCAACTATACCTGATGTTAAGGAACACTACA 360

QY 361 TATTGACAGAAAGTTCGATTTCCCTTGGAGTGTTCCTTCAAAAAGACAGCTGTTTCAATTC 420
Db 361 TATTGACAGAAAGTTCGATTTCCCTTGGAGTGTTCCTTCAAAAAGACAGCTGTTTCAATTC 420

QY 421 CCCATGAACCTCCAGTGCATAACTGTATATAGAAATATGGCAATTCAGAGGATCACTTGT 480
Db 421 CCCATGAACCTCCAGTGCATAACTGTATATAGAAATATGGCAATTCAGAGGATCACTTGT 480

QY 481 CCMAATGTATAGTGAATATTTCTTCAGTGTCAAAACCGACTATCACTTGTATATGGGC 540
Db 481 CCMAATGTATAGTGAATATTTCTTCAGTGTCAAAACCGACTATCACTTGTATATGGGC 540

QY 541 TGTATAAATAACAGAAATTTTAAATAATGTAATACCCGAAGGTATGAACCTTGATTTCCCTC 600
Db 541 TGTATAAATAACAGAAATTTTAAATAATGTAATACCCGAAGGTATGAACCTTGATTTCCCTC 600
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QY 601 ATTGCTTTAAATTTCAAATAATGAAATTAACACATGTGTTGTTTACATATATCCAGAAAAATGGA 660
Db 601 ATTGCTTTAAATTTCAAATAATGAAATTAACACATGTGTTGTTTACATATATCCAGAAAAATGGA 660

QY 661 CGTAGCTTTTCATCTCACAGGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAAAATGCA 720
Db 661 CGTAGCTTTTCATCTCACAGGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAAAATGCA 720

QY 721 GTGCCCCCTGTGATCCATTCACCTAATGATCATGTGGTCTATGAGAAAGAACCCAGGAGAG 780
Db 721 GTGCCCCCTGTGATCCATTCACCTAATGATCATGTGGTCTATGAGAAAGAACCCAGGAGAG 780

QY 781 GAGCTACTCATTTCCCTGTACGCTCTATTTTACTGTTTCTGATGGATTTCTCGCAATGAGGTT 840
Db 781 GAGCTACTCATTTCCCTGTACGCTCTATTTTACTGTTTCTGATGGATTTCTCGCAATGAGGTT 840

QY 841 TGGTGGACCATTTGATGGAAAAAACCTGATGACATCATCTATTGTATGTGTCAACATTAACGAA 900
Db 841 TGGTGGACCATTTGATGGAAAAAACCTGATGACATCATCTATTGTATGTGTCAACATTAACGAA 900

QY 901 AGTATAAGTTCATAGTAGAACACAGAGATGAAACAAAGAACTCAGATTTTGTAGCATCAAGAAA 960
Db 901 AGTATAAGTTCATAGTAGAACACAGAGATGAAACAAAGAACTCAGATTTTGTAGCATCAAGAAA 960

QY 961 GTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTCTATGTCTAGAGTGCCTCAAGGCGAA 1020
Db 961 GTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTCTATGTCTAGAGTGCCTCAAGGCGAA 1020

QY 1021 GTTGCAAGACGACCAAGGTGAAGCAGAAAGTGCAGCTCCAAAGATACACAGTGGAACTG 1080
Db 1021 GTTGCAAGACGACCAAGGTGAAGCAGAAAGTGCAGCTCCAAAGATACACAGTGGAACTG 1080

QY 1081 GCTTGTGGTTTTGGAGCCACAGCTCCTGCTAGTG 1113
Db 1081 TGCAAGGAACGTGAAGAAAAATAATTTTAGTG 1113

RESULT 14
US-10-840-138-11
; Sequence 11, Application US/10840138
; Publication No. US20040224893A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Li-Hsien
; APPLICANT: Lin, Hsin Chieh
; APPLICANT: Karow, Margaret
; TITLE OF INVENTION: Methods of Using IL-1 Antagonists to Treat Neointimal Hyperplasia
; FILE REFERENCE: REG 207A
; CURRENT APPLICATION NUMBER: US/10/840,138
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 2709
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-840-138-11

Query Match 52.0%; Score 1073; DB 8; Length 2709;
Best Local Similarity 97.8%; Pred. No. 0;
Matches 1088; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 1 ATGACACTCTGTGGTGTGTAGTGAGTCTCTACTTTTATGGAAATCCTGCAAAAGTATGCC 60
Db 1 ATGGTGTCTTCTGTGTGTGTAGTGAGTCTCTACTTTTATGGAAATCCTGCAAAAGTATGCC 60

QY 61 TCAGAACGCTGCGATGACCTGGGACTAGACACCATGAGGCAATCCAAAGTGTGAAGAT 120
Db 61 TCAGAACGCTGCGATGACCTGGGACTAGACACCATGAGGCAATCCAAAGTGTGAAGAT 120

QY 121 GAGCCAGCTCGCATCAAGTGGCCACCTCTTTGAACTCTTTGAACTCAAGTACAGCACA 180
Db 121 GAGCCAGCTCGCATCAAGTGGCCACCTCTTTGAACTCTTTGAACTCAAGTACAGCACA 180

QY 181 GCCATTTCAGCTGGCCCTTACTCTGATCTGTATTTGACTAGGACGAGCCGACCTTGAG 240
Db 181 GCCATTTCAGCTGGCCCTTACTCTGATCTGTATTTGACTAGGACGAGCCGACCTTGAG 240

QY 241 GAGCCAAATTAACCTTCGCGCTCCCGAGAACCGCATTTAGTAAAGAGAAAGATGTGCTGTGG 300
Db 241 GAGCCAAATTAACCTTCGCGCTCCCGAGAACCGCATTTAGTAAAGAGAAAGATGTGCTGTGG 300

QY 301 TTCGCGCCCACTCTCTCAATGACACTGGCAACTATACCTGATGTTAAGGAACACTACA 360
Db 301 TTCGCGCCCACTCTCTCAATGACACTGGCAACTATACCTGATGTTAAGGAACACTACA 360

QY 361 TATTGACAGAAAGTTCGATTTCCCTTGGAGTGTTCCTTCAAAAAGACAGCTGTTTCAATTC 420
Db 361 TATTGACAGAAAGTTCGATTTCCCTTGGAGTGTTCCTTCAAAAAGACAGCTGTTTCAATTC 420

QY 421 CCCATGAACCTCCAGTGCATAACTGTATATAGAAATATGGCAATTCAGAGGATCACTTGT 480
Db 421 CCCATGAACCTCCAGTGCATAACTGTATATAGAAATATGGCAATTCAGAGGATCACTTGT 480

QY 481 CCMAATGTATAGTGAATATTTCTTCAGTGTCAAAACCGACTATCACTTGTATATGGGC 540
Db 481 CCMAATGTATAGTGAATATTTCTTCAGTGTCAAAACCGACTATCACTTGTATATGGGC 540

QY 541 TGTATAAATAACAGAAATTTTAAATAATGTAATACCCGAAGGTATGAACCTTGATTTCCCTC 600
Db 541 TGTATAAATAACAGAAATTTTAAATAATGTAATACCCGAAGGTATGAACCTTGATTTCCCTC 600
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[illegible]

Search completed: December 14, 2005, 15:29:31
Job time : 1711 secs

November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New).

Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

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OM nucleic - nucleic search, using sw model

Run on: December 14, 2005, 11:41:14 ; Search time 261 Seconds
(without alignments)
3876.171 Million cell updates/sec

Title: US-10-061-727-1

Perfect score: 2064

Sequence: 1 atgacacctctggtgtgtg.....acgacttttatccctataa 2064

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4161359 seqs, 24507644 residues

Total number of hits satisfying chosen parameters: 8322718

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA New:
1: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
5: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
6: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1073	52.0	2703	7 US-11-144-987-9	Sequence 9, Appli
2	1073	52.0	2709	7 US-11-144-987-11	Sequence 11, Appl
3	1073	52.0	2709	7 US-11-144-987-13	Sequence 13, Appl
4	1069.6	51.8	2748	7 US-11-144-987-21	Sequence 21, Appl
5	1069.6	51.8	2754	7 US-11-144-987-23	Sequence 23, Appl
6	1069.6	51.8	2754	7 US-11-144-987-25	Sequence 25, Appl
7	1069.2	51.8	2733	7 US-11-144-987-1	Sequence 1, Appli
8	1017	49.3	2703	7 US-11-144-987-3	Sequence 3, Appli
9	1017	49.3	2709	7 US-11-144-987-5	Sequence 5, Appli
10	1017	49.3	2709	7 US-11-144-987-7	Sequence 7, Appli
11	1015	49.2	2748	7 US-11-144-987-15	Sequence 15, Appl
12	1015	49.2	2754	7 US-11-144-987-17	Sequence 17, Appl
13	1015	49.2	2754	7 US-11-144-987-19	Sequence 19, Appl
14	114.2	5.5	5178	6 US-10-750-185-48357	Sequence 48357, A
15	60.2	2.9	1388	6 US-10-750-185-48351	Sequence 48351, A
16	53.2	2.6	2188	6 US-10-995-561-365	Sequence 365, App
17	51.2	2.5	1612	6 US-10-750-185-48356	Sequence 48356, A
18	50.6	2.5	201	6 US-10-995-561-9887	Sequence 9887, Ap
19	48.4	2.3	54946	6 US-10-995-561-13479	Sequence 13479, A
20	39.4	1.9	201	6 US-10-995-561-78979	Sequence 78979, A
21	39.4	1.9	1197	6 US-10-821-234-731	Sequence 731, App
22	39	1.9	26772	6 US-10-995-561-13313	Sequence 13313, A
23	38.4	1.9	645179	6 US-10-995-561-13293	Sequence 13293, A

ALIGNMENTS

RESULT 1

US-11-144-987-9
; Sequence 9, Application US/11144987
; Publication No. US20050272655A1
; GENERAL INFORMATION:
; APPLICANT: Mellis, Scott
; APPLICANT: Karow, Margaret
; APPLICANT: Yancopoulos, George
; APPLICANT: Papadopoulos, Joanne
; TITLE OF INVENTION: Methods of Using IL-1 Antagonists to Treat Autoinflammatory Disease
; FILE REFERENCE: REG 2090A
; CURRENT APPLICATION NUMBER: US/11/144,987
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: 60/577,023
; PRIOR FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 2703
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-144-987-9

Query Match 52.0%; Score 1073; DB 7; Length 2703;
Best Local Similarity 97.8%; Pred. No. 0;
Matches 1088; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
QY 1 ATGACACTTCTGTGGTGTGTAGTAGTCTCTACTTTTATGGAATCTCTGCAAGTGATGCC 60
|||
Db 1 ATGGTCTTCTGTGGTGTGTAGTAGTCTCTACTTTTATGGAATCTCTGCAAGTGATGCC 60
QY 61 TCAGAACGCTGCGATGACTGGGGACTAGACACCATCAGGCAATCCAAAGTGTGTAAGAT 120
61 TCAGAACGCTGCGATGACTGGGGACTAGACACCATCAGGCAATCCAAAGTGTGTAAGAT 120
QY 121 GAGCCAGCTCGCATCAGTGGCCCACTTTTGAACACTTTTGAATTTCAACTACAGCACA 180
121 GAGCCAGCTCGCATCAGTGGCCCACTTTTGAACACTTTTGAATTTCAACTACAGCACA 180
QY 181 GCCCATTTAGCTGGCCCTTACTCTGATCTGATTTGAGCTAGGAGGACCGGGACCTTGAG 240
181 GCCCATTTAGCTGGCCCTTACTCTGATCTGATTTGAGCTAGGAGGACCGGGACCTTGAG 240
QY 241 GAGCCAAATTAACCTCCGCTCCCGGAGAACCGGATTTAGTAAAGAGAAAGATGTGCTGTGG 300
241 GAGCCAAATTAACCTCCGCTCCCGGAGAACCGGATTTAGTAAAGAGAAAGATGTGCTGTGG 300

Db 901 AGTATAAGTCATAGTAGAACAAGAGATGAACAAGAACTCAGATTTTGGAGCATCAAGAA 960
Qy 961 GTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTATGATGAGTGGCAAGGGGAA 1020
Db 961 GTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTATGATGAGTGGCAAGGGGAA 1020
Qy 1021 GTTGCCAAAGCAGCAAGGTGAAGCAGAGAGTGCAGCTCCAAAGATACACAGTGGAACTG 1080
Db 1021 GTTGCCAAAGCAGCAAGGTGAAGCAGAGAGTGCAGCTCCAAAGATACACAGTGGAA 1080
Qy 1081 GCTTGTGTTTTGGAGCCACAGTCCCTGCTAGTG 1113
Db 1081 TGCAAGGAACCTGAAGAAAAATAATTTTAGTG 1113

RESULT 3

US-11-144-987-13
; Sequence 13, Application US/11144987
; Publication No. US20050272655A1
; GENERAL INFORMATION:
; APPLICANT: Mellis, Scott
; APPLICANT: Karow, Margaret
; APPLICANT: Yancopoulos, George
; APPLICANT: Papadopoulos, Joanne
; TITLE OF INVENTION: Methods of Using IL-1 Antagonists to Treat Autoinflammatory Disease
; FILE REFERENCE: REG 2090A
; CURRENT APPLICATION NUMBER: US/11/144,987
; PRIOR FILING DATE: 2005-06-03
; PRIOR FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 2709
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-144-987-13

Query Match 52.08; Score 1073; DB 7; Length 2709;
Best Local Similarity 97.8%; Pred. No. 0;
Matches 1088; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

Qy 1 ATGACACTTCTGTGGTGTAGTGAGTCTCTACTTTTATGAAATCCTGCAAGTGTATGCC 60
Db 1 ATGGTGTCTGTGGTGTAGTGAGTCTCTACTTTTATGAAATCCTGCAAGTGTATGCC 60
Qy 61 TCAGAACGCTGCGATGACTGGGACTAGACACCATGAGGCAAAATCCAAGTGTGTTGAAGAT 120
Db 61 TCAGAACGCTGCGATGACTGGGACTAGACACCATGAGGCAAAATCCAAGTGTGTTGAAGAT 120
Qy 121 GAGCCAGCTCGCATCAAGTGCACCTCTTTGAACTCTTTGAAATCAACTACAGCACA 180
Db 121 GAGCCAGCTCGCATCAAGTGCACCTCTTTGAACTCTTTGAAATCAACTACAGCACA 180
Qy 181 GCCATTACAGTGGCCCTTACTCTGTATCTGTGTTGAGTACTAGGAGGACCGGACCTTGAG 240
Db 181 GCCATTACAGTGGCCCTTACTCTGTATCTGTGTTGAGTACTAGGAGGACCGGACCTTGAG 240
Qy 241 GAGCCAAATTAATTTCCGCTTCCCGAGAACCGCATTTAGTAGGAGAAAGATGTGCTGTGG 300
Db 241 GAGCCAAATTAATTTCCGCTTCCCGAGAACCGCATTTAGTAGGAGAAAGATGTGCTGTGG 300
Qy 301 TTCGGGCCACTCTCCTCAATGACATGACATGGCAACTATACCTGCATGTTAAGGAACACTACA 360
Db 301 TTCGGGCCACTCTCCTCAATGACATGACATGGCAACTATACCTGCATGTTAAGGAACACTACA 360
Qy 361 TATTGACGAAAGTTGCAATTTCCCTTGGAGTTGTTCAAAAAGACAGCTGTTTCAATTCC 420
Db 361 TATTGACGAAAGTTGCAATTTCCCTTGGAGTTGTTCAAAAAGACAGCTGTTTCAATTCC 420
Qy 421 CCCATGAACCTCCAGTGCATAAATCTGTATATAGAAATATGGCATTCAGAGGATCACTTGT 480

Db 421 CCCATGAACCTCCAGTGCATAAATCTGTATATAGAAATATGGCATTCAGAGGATCACTTGT 480
Qy 481 CCAAAATGTAGATGGATATTTTCCCTTCAGTGTCAAAACCGACTATCACTTGGTATATGGC 540
Db 481 CCAAAATGTAGATGGATATTTTCCCTTCAGTGTCAAAACCGACTATCACTTGGTATATGGC 540
Qy 541 TGTATTAAAAATACAGAAATTTTAAATATATATACCCGAAAGGTATGAATCTTGAGTTTCCCTC 600
Db 541 TGTATTAAAAATACAGAAATTTTAAATATATATACCCGAAAGGTATGAATCTTGAGTTTCCCTC 600
Qy 601 ATTGCCTTAATTTTCAAAATATGAAATTTACATGATGTTTACATATCCAGAAAAATGGA 660
Db 601 ATTGCCTTAATTTTCAAAATATGAAATTTACATGATGTTTACATATCCAGAAAAATGGA 660
Qy 661 CGTACGTTTCATCTCACCAGGACTCTGACGTGTAAGGTAGTAGGCTCTCCAAAAAATGCA 720
Db 661 CGTACGTTTCATCTCACCAGGACTCTGACGTGTAAGGTAGTAGGCTCTCCAAAAAATGCA 720
Qy 721 GTGCCCCCTGTGATCCATTCACCTAATGATCATGTGTCTATGAGAAAGAACCCAGGAGAG 780
Db 721 GTGCCCCCTGTGATCCATTCACCTAATGATCATGTGTCTATGAGAAAGAACCCAGGAGAG 780
Qy 781 GAGCTACTATCCCTGTACGGTCTATTTTAGTATTTCTGTATGATGATTCGCAATGAGTT 840
Db 781 GAGCTACTATCCCTGTACGGTCTATTTTAGTATTTCTGTATGATGATTCGCAATGAGTT 840
Qy 841 TGGTGCACCATTCATCGAAAAAACCTGATGACATCACTATTGATGTCACCATTAACGAA 900
Db 841 TGGTGCACCATTCATCGAAAAAACCTGATGATGACATCACTATTGATGTCACCATTAACGAA 900
Qy 901 AGTATAAGTCATAGTAGAACAAGAGATGAACAAGAACTCAGATTTTGGAGCATCAAGAAA 960
Db 901 AGTATAAGTCATAGTAGAACAAGAGATGAACAAGAACTCAGATTTTGGAGCATCAAGAAA 960
Qy 961 GTTACCTCTGAGGATCTCAAGCCGAGCTATGTCTGTATGCTAGAGTGCAGAAAGGGGAA 1020
Db 961 GTTACCTCTGAGGATCTCAAGCCGAGCTATGTCTGTATGCTAGAGTGCAGAAAGGGGAA 1020
Qy 1021 GTTGCCAAAGCAGCAAGGTGAAGCAGAGTGCAGCTCCAAAGATACACAGTGGAACTG 1080
Db 1021 GTTGCCAAAGCAGCAAGGTGAAGCAGAGTGCAGCTCCAAAGATACACAGTGGAA 1080
Qy 1081 GCTTGTGTTTTGGAGCCACAGTCCCTGCTAGTG 1113
Db 1081 TGCAAGGAACCTGAAGAAAAATAATTTTAGTG 1113

RESULT 4

US-11-144-987-21
; Sequence 21, Application US/11144987
; Publication No. US20050272655A1
; GENERAL INFORMATION:
; APPLICANT: Mellis, Scott
; APPLICANT: Karow, Margaret
; APPLICANT: Yancopoulos, George
; APPLICANT: Papadopoulos, Joanne
; TITLE OF INVENTION: Methods of Using IL-1 Antagonists to Treat Autoinflammatory Disease
; FILE REFERENCE: REG 2090A
; CURRENT APPLICATION NUMBER: US/11/144,987
; PRIOR FILING DATE: 2005-06-03
; PRIOR FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 2748
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-144-987-21

Query Match 51.8%; Score 1069.6; DB 7; Length 2748;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1072; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ATGACACTTCTGTGGTGTGTAGTCTCTACTTTTATGGAATCTCGAAAGTGATGCC 60
Db |||||
1 ATGGTGTCTGTGGTGTGTAGTCTCTACTTTTATGGAATCTCGAAAGTGATGCC 60
QY 61 TCAGAACGCTGCATGACTGGGACTAGACACCATGAGGCAATCAAGTGTGAGAT 120
Db |||||
61 TCAGAACGCTGCATGACTGGGACTAGACACCATGAGGCAATCAAGTGTGAGAT 120
QY 121 GAGCCAGCTCGCATCAAGTGGCCACTCTTTGAACACTCTTTGAAATTCAACTACAGACA 180
Db |||||
121 GAGCCAGCTCGCATCAAGTGGCCACTCTTTGAACACTCTTTGAAATTCAACTACAGACA 180
QY 181 GCCCATTCAGCTGGCCCTTACTCTGATCTGTATTGGACTAGGAGGACCGGACCTTGAG 240
Db |||||
181 GCCCATTCAGCTGGCCCTTACTCTGATCTGTATTGGACTAGGAGGACCGGACCTTGAG 240
QY 241 GAGCCAAATTAACCTTCGCGCTCCCGAGAACCGCATTAGTAAGGAGAAAGATGTCTGTGG 300
Db |||||
241 GAGCCAAATTAACCTTCGCGCTCCCGAGAACCGCATTAGTAAGGAGAAAGATGTCTGTGG 300
QY 301 TTCGCGCCCACTCTCTCAATGACACTGGCAACTATACCTGCAATGTTAAGGAACACTACA 360
Db |||||
301 TTCGCGCCCACTCTCTCAATGACACTGGCAACTATACCTGCAATGTTAAGGAACACTACA 360
QY 361 TATTGAGCAAAAGTTGCATTTCCCTTTGGAAGTTGTTCAAAAAGACAGCTGTTTCAATTC 420
Db |||||
361 TATTGAGCAAAAGTTGCATTTCCCTTTGGAAGTTGTTCAAAAAGACAGCTGTTTCAATTC 420
QY 421 CCCATGAAACTCCAGTGGCAATTAAGTATAGAAATATGGAATTCAGAGGATCACTTGT 480
Db |||||
421 CCCATGAAACTCCAGTGGCAATTAAGTATAGAAATATGGAATTCAGAGGATCACTTGT 480
QY 481 CCAAAATGAGTGGATATTTTCTTCCAGTGTCAAAACCGACTATCACTTGGTATATGGGC 540
Db |||||
481 CCAAAATGAGTGGATATTTTCTTCCAGTGTCAAAACCGACTATCACTTGGTATATGGGC 540
QY 541 TGTATATAAATACAGAAATTTTAAATGTAATACCCGAGGATGAACTTTGAGTTCCTC 600
Db |||||
541 TGTATATAAATACAGAAATTTTAAATGTAATACCCGAGGATGAACTTTGAGTTCCTC 600
QY 601 ATTGCGCTTAATTTCAAATTAATGAAATTAACATGATGTTGTTTACATATCCAGAAAAATGGA 660
Db |||||
601 ATTGCGCTTAATTTCAAATTAATGAAATTAACATGATGTTGTTTACATATCCAGAAAAATGGA 660
QY 661 CGTAGCTTTTCATCTCACCGAGCTCTGACTGTAAGGATAGTAGGCTCTCAAAAATGCA 720
Db |||||
661 CGTAGCTTTTCATCTCACCGAGCTCTGACTGTAAGGATAGTAGGCTCTCAAAAATGCA 720
QY 721 GTGCCCCCTGTGATCCATTCACTAATGATCATGTGGTCTATGAGAAAGAACCCAGAGAG 780
Db |||||
721 GTGCCCCCTGTGATCCATTCACTAATGATCATGTGGTCTATGAGAAAGAACCCAGAGAG 780
QY 781 GAGCTACTCATTTCCCTGTACGGTCTATTTTAGTTTCTGATGGATTTCTGCAATGAGTT 840
Db |||||
781 GAGCTACTCATTTCCCTGTACGGTCTATTTTAGTTTCTGATGGATTTCTGCAATGAGTT 840
QY 841 TGGTGGACCAATTGATGGAAGAAACCTGATGACATCACTATTGATGTCACCAATTAACGAA 900
Db |||||
841 TGGTGGACCAATTGATGGAAGAAACCTGATGACATCACTATTGATGTCACCAATTAACGAA 900
QY 901 AGTATAAGTCATAGTAGAAGCAGAAAGTAAACCAAGAACTCAGATTTTGGACATCAAGAAA 960
Db |||||
901 AGTATAAGTCATAGTAGAAGCAGAAAGTAAACCAAGAACTCAGATTTTGGACATCAAGAAA 960
QY 961 GTTACCTCTGAGGATCTCAAGCCGAGTATGTCTGTCTGCTAGAGATGCGCAAGCGGAA 1020
Db |||||
961 GTTACCTCTGAGGATCTCAAGCCGAGTATGTCTGTCTGCTAGAGATGCGCAAGCGGAA 1020
QY 1021 GTTGCCAAAGCAGCCAGGTTGAAGCAAGAAAGTGCCAGCTCCAAGATACACAGTGCA 1076
Db |||||
1021 GTTGCCAAAGCAGCCAGGTTGAAGCAAGAAAGTGCCAGCTCCAAGATACACAGTGCA 1076

RESULT 5
US-11-144-987-23
; Sequence 23, Application US/11144987
; Publication No. US20050272655A1
; GENERAL INFORMATION:
; APPLICANT: Mellis, Scott
; APPLICANT: Karow, Margaret
; APPLICANT: Yancopoulos, George
; APPLICANT: Papadopoulos, Joanne
; TITLE OF INVENTION: Methods of Using IL-1 Antagonists to Treat Autoinflammatory Dise
; FILE REFERENCE: REG 2030A
; CURRENT APPLICATION NUMBER: US/11/144,987
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: 60/577,023
; PRIOR FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 2754
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-144-987-23

Query Match 51.8%; Score 1069.6; DB 7; Length 2754;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1072; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ATGACACTTCTGTGTGTGTAGTCTCTACTTTTATGGAATCTCGAAAGTGATGCC 60
Db |||||
1 ATGGTGTCTTCTGTGTGTGTAGTCTCTACTTTTATGGAATCTCGAAAGTGATGCC 60
QY 61 TCAGAACGCTGCGATGACTGGGGAAGCTAGACACCATGAGGCAATCAAGTGTGGAAGAT 120
Db |||||
61 TCAGAACGCTGCGATGACTGGGGAAGCTAGACACCATGAGGCAATCAAGTGTGGAAGAT 120
QY 121 GAGCCAGCTCGCATCAAGTGGCCACTCTTTGAACTCTTTGAAATTCAACTACAGACA 180
Db |||||
121 GAGCCAGCTCGCATCAAGTGGCCACTCTTTGAACTCTTTGAAATTCAACTACAGACA 180
QY 181 GCCCATTCAGCTGGCCCTTACTCTGATCTGTATTGGACTAGGAGGACCGGACCTTGAG 240
Db |||||
181 GCCCATTCAGCTGGCCCTTACTCTGATCTGTATTGGACTAGGAGGACCGGACCTTGAG 240
QY 241 GAGCCAAATTAACCTTCGCGCTCCCGAGAACCCGATTAGTAAGGAGAAAGATGTCTGTGG 300
Db |||||
241 GAGCCAAATTAACCTTCGCGCTCCCGAGAACCCGATTAGTAAGGAGAAAGATGTCTGTGG 300
QY 301 TTCGCGCCCACTCTCTCAATGACACTGGCAACTATGGAATTCAGAGGACACTACA 360
Db |||||
301 TTCGCGCCCACTCTCTCAATGACACTGGCAACTATGGAATTCAGAGGACACTACA 360
QY 361 TATTGAGCAAAAGTTGCATTTCCCTTTGGAAGTTGTTCAAAAAGACAGCTGTTTCAATTC 420
Db |||||
361 TATTGAGCAAAAGTTGCATTTCCCTTTGGAAGTTGTTCAAAAAGACAGCTGTTTCAATTC 420
QY 421 CCCATGAAACTCCAGTGGCAATTAAGTATAGAAATATGGAATTCAGAGGATCACTTGT 480
Db |||||
421 CCCATGAAACTCCAGTGGCAATTAAGTATAGAAATATGGAATTCAGAGGATCACTTGT 480
QY 481 CCAAAATGAGTGGATATTTTCTTCCAGTGTCAAAACCGACTATCACTTGGTATATGGGC 540
Db |||||
481 CCAAAATGAGTGGATATTTTCTTCCAGTGTCAAAACCGACTATCACTTGGTATATGGGC 540
QY 541 TGTATATAAATACAGAAATTTTAAATGTAATACCCGAGGATGAACTTTGAGTTCCTC 600
Db |||||
541 TGTATATAAATACAGAAATTTTAAATGTAATACCCGAGGATGAACTTTGAGTTCCTC 600
QY 601 ATTGCGCTTAATTTCAAATTAATGAAATTAACATGATGTTGTTTACATATCCAGAAAAATGGA 660
Db |||||
601 ATTGCGCTTAATTTCAAATTAATGAAATTAACATGATGTTGTTTACATATCCAGAAAAATGGA 660
QY 661 CGTAGCTTTTCATCTCACCGAGCTCTGACTGTAAGGATAGTAGGCTCTCAAAAATGCA 720
Db |||||
661 CGTAGCTTTTCATCTCACCGAGCTCTGACTGTAAGGATAGTAGGCTCTCAAAAATGCA 720

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Db 661 CGTACGTTTCATCTCACCAGGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAATGCA 720
Qy 721 GTGCCCCCTGTGATCCATTACCTAATGATCATGTGTCTATGAGAAAGAACACAGGAG 780
Db 721 GTGCCCCCTGTGATCCATTACCTAATGATCATGTGTCTATGAGAAAGAACACAGGAG 780
Qy 781 GAGCTACTCATTCCTCTGACGGTCTATTATTAGTTTCTGATGGATTCTCGCAATGAGTT 840
Db 781 GAGCTACTCATTCCTCTGACGGTCTATTATTAGTTTCTGATGGATTCTCGCAATGAGTT 840
Qy 841 TGTGGACCAATTGATGGAAGAAAAACCTGATGACATCACTATTGATGTCACCATTAACGAA 900
Db 841 TGTGGACCAATTGATGGAAGAAAAACCTGATGACATCACTATTGATGTCACCATTAACGAA 900
Qy 901 AGTATAGTCATAGTAGAAGAGAGATGAACAGAACTCAGATTTTGAGCATCAAGAAA 960
Db 901 AGTATAGTCATAGTAGAAGAGATGAACAGAACTCAGATTTTGAGCATCAAGAAA 960
Qy 961 GTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTCATGCTAGAGTGCCAAAGGCGAA 1020
Db 961 GTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTCATGCTAGAGTGCCAAAGGCGAA 1020
Qy 1021 GTTGCCAAAGCAGCAGGAGGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1076
Db 1021 GTTGCCAAAGCAGCAGGAGGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
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RESULT 6

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US-11-144-987-25
; Sequence 25, Application US/11144987
; Publication No. US20050272655A1
; GENERAL INFORMATION:
; APPLICANT: Mellis, Scott
; APPLICANT: Karow, Margaret
; APPLICANT: Yancopoulos, George
; APPLICANT: Papadopoulos, Joanne
; TITLE OF INVENTION: Methods of Using IL-1 Antagonists to Treat Autoinflammatory Disease
; FILE REFERENCE: REG 2090A
; CURRENT APPLICATION NUMBER: US/11/144,987
; CURRENT FILING DATE: 2005-06-03
; PRIOR FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 2754
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-144-987-25
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Query Match 51.8%; Score 1069.6; DB 7; Length 2754;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1072; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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Qy 1 ATGACACTCTGTGGTGTGTAGTGAGTCTCTACTTTTATGGAATCCTGCAAGATGATGCC 60
Db 1 ATGCTGTTCTGTGGTGTGTAGTGAGTCTCTACTTTTATGGAATCCTGCAAGATGATGCC 60
Qy 61 TCAGAACGCTGCGATGACTCGGGGACTAGACACCATGAGGCAAAATCCAAGTGTGTTGAAGAT 120
Db 61 TCAGAACGCTGCGATGACTCGGGGACTAGACACCATGAGGCAAAATCCAAGTGTGTTGAAGAT 120
Qy 121 GAGCCAGCTCGCATCAAGTCCCACTCTTTGAACACTCTTTGAATTCACACTACAGCACA 180
Db 121 GAGCCAGCTCGCATCAAGTCCCACTCTTTGAACACTCTTTGAATTCACACTACAGCACA 180
Qy 181 GCCATTACGCTGGCCTTACTCTGATCTGTATTGAGTACGAGGACCGGGACCTTTGAG 240
Db 181 GCCATTACGCTGGCCTTACTCTGATCTGTATTGAGTACGAGGACCGGGACCTTTGAG 240
Qy 241 GAGCCCAATTAATCTCCGCTCTCCCGAGAACCGCAATTAGTAAGGAGAAAGATGTGCTGTGG 300
Db 241 GAGCCCAATTAATCTCCGCTCTCCCGAGAACCGCAATTAGTAAGGAGAAAGATGTGCTGTGG 300
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```
Db 241 GAGCCCAATTAATCTCCGCTCTCCCGAGAACCGCAATTAGTAAGGAGAAAGATGTGCTGTGG 300
Qy 301 TTCCGGCCCCACTCTCTCAATGACACTGGCAACTATACCTGCACTGTGTAAGGAACACTACA 360
Db 301 TTCCGGCCCCACTCTCTCAATGACACTGGCAACTATACCTGCACTGTGTAAGGAACACTACA 360
Qy 361 TATTGACAGCAAAAGTTGCAATTTCCCTTGGAAAGTGTGTTCAAAAAGACAGCTGTTTCAATTC 420
Db 361 TATTGACAGCAAAAGTTGCAATTTCCCTTGGAAAGTGTGTTCAAAAAGACAGCTGTTTCAATTC 420
Qy 421 CCATGAAACTCCCATGTCATAACTGTATATAGATAATGCGCATTTGAGAGATCACTTGT 480
Db 421 CCATGAAACTCCCATGTCATAACTGTATATAGATAATGCGCATTTGAGAGATCACTTGT 480
Qy 481 CCAAAATGATAGTGGATATTTTCCCTCCAGTGTCAAAACCGACTATCACTTGGTATATGGGC 540
Db 481 CCAAAATGATAGTGGATATTTTCCCTCCAGTGTCAAAACCGACTATCACTTGGTATATGGGC 540
Qy 541 TGTATATAAATACAGAAATTTTAAATAATGTAATACCCGAAAGGTATGAACCTTTGAGTTTCCCTC 600
Db 541 TGTATATAAATACAGAAATTTTAAATAATGTAATACCCGAAAGGTATGAACCTTTGAGTTTCCCTC 600
Qy 601 ATTGCTCTTAATTTCAAAATTAATGGAATTAACATGTGTTGTTACATATCCAGAAAAATGGA 660
Db 601 ATTGCTCTTAATTTCAAAATTAATGGAATTAACATGTGTTGTTACATATCCAGAAAAATGGA 660
Qy 661 CGTACGTTTCATCTCACCAGGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAATGCA 720
Db 661 CGTACGTTTCATCTCACCAGGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAATGCA 720
Qy 721 GTGCCCCCTGTGATCCATTACCTAATGATCATGTGTCTATGAGAAAGAACACAGGAGAG 780
Db 721 GTGCCCCCTGTGATCCATTACCTAATGATCATGTGTCTATGAGAAAGAACACAGGAGAG 780
Qy 781 GAGCTACTCATTCCTCTGATCGGTCATTTTAGTTTCTGATGATTTCTGCAATGAGTT 840
Db 781 GAGCTACTCATTCCTCTGATCGGTCATTTTAGTTTCTGATGATTTCTGCAATGAGTT 840
Qy 841 TGTGGACCAATTGATGGAAGAAAAACCTGATGACATCACTATTGATGTCACCATTAACGAA 900
Db 841 TGTGGACCAATTGATGGAAGAAAAACCTGATGACATCACTATTGATGTCACCATTAACGAA 900
Qy 901 AGTATAAGTCATAGTAGAAGAGATGAACAGAACTCAGATTTTGAGCATCAAGAAA 960
Db 901 AGTATAAGTCATAGTAGAAGAGATGAACAGAACTCAGATTTTGAGCATCAAGAAA 960
Qy 961 GTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTCATGCTAGAGTGCCAAAGGCGAA 1020
Db 961 GTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTCATGCTAGAGTGCCAAAGGCGAA 1020
Qy 1021 GTTGCCAAAGCAGCAGGAGGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1076
Db 1021 GTTGCCAAAGCAGCAGGAGGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
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RESULT 7

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US-11-144-987-1
; Sequence 1, Application US/11144987
; Publication No. US20050272655A1
; GENERAL INFORMATION:
; APPLICANT: Mellis, Scott
; APPLICANT: Karow, Margaret
; APPLICANT: Yancopoulos, George
; APPLICANT: Papadopoulos, Joanne
; TITLE OF INVENTION: Methods of Using IL-1 Antagonists to Treat Autoinflammatory Disease
; FILE REFERENCE: REG 2090A
; CURRENT APPLICATION NUMBER: US/11/144,987
; CURRENT FILING DATE: 2005-06-03
; PRIOR FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
```

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; LENGTH: 2733
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-144-987-1

Query Match      51.8%; Score 1069.2; DB 7; Length 2733;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1071; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGACACTCTGTGGTGTGTAGTGTCTCTACTTTTATGGAATCCTGCAAAAGTGATGCC 60
   |||
Db 1 ATGGTCTTCTGTGGTGTGTAGTGTCTCTACTTTTATGGAATCCTGCAAAAGTGATGCC 60

QY 61 TCAGAACGCTGCGATGACTGGGACTAGACACCATGAGGCAAAATCCAAGTGTTTGAAGAT 120
   |||
Db 61 TCAGAACGCTGCGATGACTGGGACTAGACACCATGAGGCAAAATCCAAGTGTTTGAAGAT 120

QY 121 GAGCAGCTCGCATCAAGTGGCCACTCTTTTGAACACTTCTTGAATTTCAACTACAGCACA 180
   |||
Db 121 GAGCAGCTCGCATCAAGTGGCCACTCTTTTGAACACTTCTTGAATTTCAACTACAGCACA 180

QY 181 GCCCATTACAGTGGCCCTTACTCTGATCTGATTTGGACTAGCAGGACCGGACCTTGAG 240
   |||
Db 181 GCCCATTACAGTGGCCCTTACTCTGATCTGATTTGGACTAGCAGGACCGGACCTTGAG 240

QY 241 GAGCCAAATTAACCTCCGCTCCCGAGAACCGCATTTAGTAAGGAGAAAGATGTGCTGG 300
   |||
Db 241 GAGCCAAATTAACCTCCGCTCCCGAGAACCGCATTTAGTAAGGAGAAAGATGTGCTGG 300

QY 301 TTCCGGCCCACTCTCCTCAATGACACTGGCAACTATACCTGATGTTAAGGAACACTACA 360
   |||
Db 301 TTCCGGCCCACTCTCCTCAATGACACTGGCAACTATACCTGATGTTAAGGAACACTACA 360

QY 361 TATTGACAGAAAGTTCATTTCCCTTGGAGTGTGTTCAAAAAGACAGCTGTTTCAATTC 420
   |||
Db 361 TATTGACAGAAAGTTCATTTCCCTTGGAGTGTGTTCAAAAAGACAGCTGTTTCAATTC 420

QY 421 CCCATGAAACTCCAGTGCATAAATCTGTATATAGAAATATGGCAATTCAGAGGATCACTTGT 480
   |||
Db 421 CCCATGAAACTCCAGTGCATAAATCTGTATATAGAAATATGGCAATTCAGAGGATCACTTGT 480

QY 481 CCAATGTATAGATGATTTTCTCCAGTGTCAAAACCGACTATCACTTTGGTATATGGGC 540
   |||
Db 481 CCAATGTATAGATGATTTTCTCCAGTGTCAAAACCGACTATCACTTTGGTATATGGGC 540

QY 541 TGTATATAAATACAGAAATTTTAAATATGTAATACCGAAGGTATGAACCTTGAAGTTTCTC 600
   |||
Db 541 TGTATATAAATACAGAAATTTTAAATATGTAATACCGAAGGTATGAACCTTGAAGTTTCTC 600

QY 601 ATTGCCTTAATTTCAAATTAATGAAATTAACATGTTGTTGTATACATATCCAGAAATGGA 660
   |||
Db 601 ATTGCCTTAATTTCAAATTAATGAAATTAACATGTTGTTGTATACATATCCAGAAATGGA 660

QY 661 CGTACGTTTCATCTCACCAGGACTGACTGTAAAGGTAGTAGGCTCTCAAAAATGCA 720
   |||
Db 661 CGTACGTTTCATCTCACCAGGACTGACTGTAAAGGTAGTAGGCTCTCAAAAATGCA 720

QY 721 GTGCCCTTGATGCATTCATTCATATGATCATGTGGTCTATGAGAAAGAACCCAGAGAG 780
   |||
Db 721 GTGCCCTTGATGCATTCATTCATATGATCATGTGGTCTATGAGAAAGAACCCAGAGAG 780

QY 781 GAGCTACTCATTTCCCTGTACGGTCTATTTTGTGTTTCTGATGGAATTCGCAATGAGGTT 840
   |||
Db 781 GAGCTACTCATTTCCCTGTACGGTCTATTTTGTGTTTCTGATGGAATTCGCAATGAGGTT 840

QY 841 TGGTGGACCATTTGATGGAAAAAACCCTGATGATCATCACTATTGATGTACCAATTAACGAA 900
   |||
Db 841 TGGTGGACCATTTGATGGAAAAAACCCTGATGATCATCACTATTGATGTACCAATTAACGAA 900

QY 901 AGTATAAGTCATAGTAGAAGATGAAACCAAGAACTCAGATTTTGTAGCATCAAGAAA 960
   |||
Db 901 AGTATAAGTCATAGTAGAAGATGAAACCAAGAACTCAGATTTTGTAGCATCAAGAAA 960
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QY 961 GTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTATGCTAGAGTCCCAAAGCGAA 1020
   |||
Db 961 GTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTATGCTAGAGTCCCAAAGCGAA 1020

QY 1021 GTTGCCAAAGCAGCCCAAGGTGAGCAGAAAGTGCCAGCTCCCAAGATACACAGTG 1074
   |||
Db 1021 GTTGCCAAAGCAGCCCAAGGTGAGCAGAAAGTGCCAGCTCCCAAGATACACAGTG 1074

RESULT 8
US-11-144-987-3
; Sequence 3, Application US/11144987
; Publication No. US2005027265S1
; GENERAL INFORMATION:
; APPLICANT: Mellis, Scott
; APPLICANT: Karow, Margaret
; APPLICANT: Yancopoulos, George
; APPLICANT: Papadopoulos, Joanne
; TITLE OF INVENTION: Methods of Using IL-1 Antagonists to Treat Autoinflammatory Dise
; FILE REFERENCE: REG 2090A
; CURRENT APPLICATION NUMBER: US/11/144,987
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: 60/577,023
; PRIOR FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 2703
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-144-987-3

Query Match      49.3%; Score 1017; DB 7; Length 2703;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 TCAGAACCTGCGATGACTGGGGACTAGACACCATGAGGCAAAATCCAAGTGTTTGAAGAT 120
   |||
Db 997 TCAGAACCTGCGATGACTGGGGACTAGACACCATGAGGCAAAATCCAAGTGTTTGAAGAT 1056

QY 121 GAGCAGCTCGCATCAAGTGGCCACTCTTTGAACTTCTTGAATTTCAACTACAGCACA 180
   |||
Db 1057 GAGCAGCTCGCATCAAGTGGCCACTCTTTGAACTTCTTGAATTTCAACTACAGCACA 1116

QY 181 GCCCATTACAGTGGCTTACTCTGATCTGGTATTGGACTAGGACGACCGGACCTTGAG 240
   |||
Db 1117 GCCCATTACAGTGGCTTACTCTGATCTGGTATTGGACTAGGACGACCGGACCTTGAG 1176

QY 241 GAGCCAAATTAACCTCCGCTCCCGAGAACCCGATTTAGTAAAGGAAAGATGTGCTGG 300
   |||
Db 1177 GAGCCAAATTAACCTCCGCTCCCGAGAACCCGATTTAGTAAAGGAAAGATGTGCTGG 1236

QY 301 TTCCGGCCCACTCTCCTCAATGACACTGGCACTACTGCTGATGTTTCAAAAAGACAGCTGTTTCAATTC 420
   |||
Db 1237 TTCCGGCCCACTCTCCTCAATGACACTGGCACTACTGCTGATGTTTAAAGGAACACTACA 1296

QY 361 TATTGACAGAAAGTGTGCAATTTCCCTTGGAAAGTGTGTTCAAAAAGACAGCTGTTTCAATTC 420
   |||
Db 1297 TATTGACAGAAAGTGTGCAATTTCCCTTGGAAAGTGTGTTCAAAAAGACAGCTGTTTCAATTC 1356

QY 421 CCCATGAAATCCCAAGTGCATAAACTGTATATAGAAATATGGCAATTCAGAGGATCACTTGT 480
   |||
Db 1357 CCCATGAAATCCCAAGTGCATAAACTGTATATAGAAATATGGCAATTCAGAGGATCACTTGT 1416

QY 481 CCAATGTAGATGGATATTTTCTCCAGTGTCAACCGACTATCACTTTGGTATATGGGC 540
   |||
Db 1417 CCAATGTAGATGGATATTTTCTCCAGTGTCAACCGACTATCACTTTGGTATATGGGC 1476

QY 541 TGTATATAAATACAGAAATTTTAAATATGTAATACCGAAGGTATGAACCTTGTGTTTCTC 600
   |||
Db 1477 TGTATATAAATACAGAAATTTTAAATATGTAATACCGAAGGTATGAACCTTGTGTTTCTC 1536

QY 601 ATTGCTCTAATTTCAAATAATGGAATTTACACATGTGTTGTGTACATATCCAGAAATGGA 660
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Db 1537 ATTGCCCTTAATTTCAATAATGGAATTTACACATGTGTTGTATACATATCCAGAAATGGA 1596
QY 661 CGTACGTTTCATCTCACCAGGACTCTGACTGTAAAGTAGTAGGCTCTCAAAAAATGCA 720
Db 1597 CGTACGTTTCATCTCACCAGGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAAATGCA 1656
QY 721 GTGCCCCCTGTGATCCATTCACCTAAATGATCATGTGGTCTATGAGAAAGAACACAGGAG 780
Db 1657 GTGCCCCCTGTGATCCATTCACCTAAATGATCATGTGGTCTATGAGAAAGAACACAGGAG 1716
QY 781 GAGCTACTCATTCCTCTGACGGTCTATTTTAGTTTCTGATGGATTCTCGCAATGAGTT 840
Db 1717 GAGCTACTCATTCCTCTGACGGTCTATTTTAGTTTCTGATGGATTCTCGCAATGAGTT 1776
QY 841 TGGTGGACCAATGATGAAAAAACCTGATGACATCACTATTGATGTCACCATTAAGCAA 900
Db 1777 TGGTGGACCAATGATGAAAAAACCTGATGACATCACTATTGATGTCACCATTAAGCAA 1836
QY 901 AGTATAAGTCATAGTAGAAGAGATGAAACAGAACTCAGATTTTGGAGCAACAAGAA 960
Db 1837 AGTATAAGTCATAGTAGAAGAGATGAAACAGAACTCAGATTTTGGAGCAACAAGAA 1896
QY 961 GTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTCATGCTAGAGTGCCAAAGCGCAA 1020
Db 1897 GTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTCATGCTAGAGTGCCAAAGCGCAA 1956
QY 1021 GTTGCCAAAGCAGCAAGGTGAAGCAGAAAGTGCCAGCTCAAGATACACAGTGGAA 1077
Db 1957 GTTGCCAAAGCAGCAAGGTGAAGCAGAAAGTGCCAGCTCAAGATACACAGTGGAA 2013

RESULT 9
US-11-144-987-5
; Sequence 5, Application US/11144987
; Publication No. US20050272655A1
; GENERAL INFORMATION:
; APPLICANT: Mellis, Scott
; APPLICANT: Karow, Margaret
; APPLICANT: Yancopoulos, George
; APPLICANT: Papadopoulos, Joanne
; TITLE OF INVENTION: Methods of Using IL-1 Antagonists to Treat Autoinflammatory Disea
; FILE REFERENCE: REG 2090A
; CURRENT APPLICATION NUMBER: US/11/144,987
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: 60/577,023
; PRIOR FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 2709
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-144-987-5

Query Match 49.3%; Score 1017; DB 7; Length 2709;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 TCAGAACGCTGCGATGACTGGGACTAGACACCATAGAGGCAAAATCCAAAGTGTGTTGAAGAT 120
Db 997 TCAGAACGCTGCGATGACTGGGACTAGACACCATAGAGGCAAAATCCAAAGTGTGTTGAAGAT 1056
QY 121 GAGCCAGCTCGCATCAAGTGCCCACTCTTTGAACACTCTTTGAAATTCACATCAGACACA 180
Db 1057 GAGCCAGCTCGCATCAAGTGCCCACTCTTTGAACACTCTTTGAAATTCACATCAGACACA 1116
QY 181 GCCATTTCAGTGGCCTTACTCTGATCTGTTGATGAGTGGAGGACCGGACCTTGAG 240
Db 1117 GCCATTTCAGTGGCCTTACTCTGATCTGTTGATGAGTGGAGGACCGGACCTTGAG 1176
QY 241 GAGCCAAATTAATTTCCGCTCTCCCGAGAACCGCATTAAGTAGAGGAGAAAGATGTGCTGTGG 300
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```
RESULT 10
US-11-144-987-7
; Sequence 7, Application US/11144987
; Publication No. US20050272655A1
; GENERAL INFORMATION:
; APPLICANT: Mellis, Scott
; APPLICANT: Karow, Margaret
; APPLICANT: Yancopoulos, George
; APPLICANT: Papadopoulos, Joanne
; TITLE OF INVENTION: Methods of Using IL-1 Antagonists to Treat Autoinflammatory Disea
; FILE REFERENCE: REG 2090A
; CURRENT APPLICATION NUMBER: US/11/144,987
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: 60/577,023
; PRIOR FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
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Db 1177 GAGCCAAATTAATTTCCGCTCTCCCGAGAACCGCATTAGTAGAGGAGAAAGATGTGCTGTGG 1236
QY 301 TTCCGGCCCCACCTCTCTCAATGACACTGGCAACTATACCTGCACTGTTTAAGGAACACTACA 360
Db 1237 TTCCGGCCCCACCTCTCTCAATGACACTGGCAACTATACCTGCACTGTTTAAGGAACACTACA 1296
QY 361 TATTGACGACAAAGTTGCAATTTCCCTTTGGAAGTTGTTCAAAAAGACAGCTGTTTCAATTC 420
Db 1297 TATTGACGACAAAGTTGCAATTTCCCTTTGGAAGTTGTTCAAAAAGACAGCTGTTTCAATTC 1356
QY 421 CCATGAAACTCCCGAGTGCATAAATCTGTATATAGAATATGGCAATTCAGAGGATCACTTGT 480
Db 1357 CCATGAAACTCCCGAGTGCATAAATCTGTATATAGAATATGGCAATTCAGAGGATCACTTGT 1416
QY 481 CCAAAATGATAGATGATATTTCCCTCCAGTGTCAAAACCGACTATCACTTGGTATATGGGC 540
Db 1417 CCAAAATGATAGATGATATTTCCCTCCAGTGTCAAAACCGACTATCACTTGGTATATGGGC 1476
QY 541 TGTATAAAATACAGAAATTTTAATAATACCCGAAAGGTATGAATTTGAGTTTCCCTC 600
Db 1477 TGTATAAAATACAGAAATTTTAATAATACCCGAAAGGTATGAATTTGAGTTTCCCTC 1536
QY 601 ATTCCTTTAATTTCAAAATTAATGGAATTTACACATGTGTTGTTACATATCCAGAAAAATGGA 660
Db 1537 ATTCCTTTAATTTCAAAATTAATGGAATTTACACATGTGTTGTTACATATCCAGAAAAATGGA 1596
QY 661 CGTACGTTTCATCTCACCAGGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAAATGCA 720
Db 1597 CGTACGTTTCATCTCACCAGGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAAATGCA 1656
QY 721 GTGCCCCCTGTGATCCATTCACCTAAATGATCATGTGGTCTATGAGAAAGAACACAGGAGAG 780
Db 1657 GTGCCCCCTGTGATCCATTCACCTAAATGATCATGTGGTCTATGAGAAAGAACACAGGAGAG 1716
QY 781 GAGCTACTCATTCCTCTGACGGTCTATTTTAGTTTCTGATGGATTCTCGCAATGAGTT 840
Db 1717 GAGCTACTCATTCCTCTGACGGTCTATTTTAGTTTCTGATGGATTCTCGCAATGAGTT 1776
QY 841 TGGTGGACCAATGATGAAAAAACCTGATGACATCACTATTGATGTCACCATTAAGCAA 900
Db 1777 TGGTGGACCAATGATGAAAAAACCTGATGACATCACTATTGATGTCACCATTAAGCAA 1836
QY 901 AGTATAAGTCATAGTAGAAGAGATGAAACAGAACTCAGATTTTGGAGCAACAAGAA 960
Db 1837 AGTATAAGTCATAGTAGAAGAGATGAAACAGAACTCAGATTTTGGAGCAACAAGAA 1896
QY 961 GTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTCATGCTAGAGTGCCAAAGCGCAA 1020
Db 1897 GTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTCATGCTAGAGTGCCAAAGCGCAA 1956
QY 1021 GTTGCCAAAGCAGCAAGGTGAAGCAGAAAGTGCCAGCTCAAGATACACAGTGGAA 1077
Db 1957 GTTGCCAAAGCAGCAAGGTGAAGCAGAAAGTGCCAGCTCAAGATACACAGTGGAA 2013
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; LENGTH: 2709
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-144-987-7

Query Match      49.3%; Score 1017; DB 7; Length 2709;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 TCAGAACGCTGGCATGACTGGGACTAGACACCATGAGGCAAAATCCAAGTGTGTTGAAGAT 120
Db 997 TCAGAACGCTGGCATGACTGGGACTAGACACCATGAGGCAAAATCCAAGTGTGTTGAAGAT 1056

QY 121 GAGCCAGCTCGCATCAAGTGGCCACTCTTTGAACTCTTTGAAATTCAACTACAGCACA 180
Db 1057 GAGCCAGCTCGCATCAAGTGGCCACTCTTTGAACTCTTTGAAATTCAACTACAGCACA 1116

QY 181 GCCCATTCAGCTGGCCCTTACTCTGATCTGTTATTTGACTAGGAGGACCGGACCTTGAG 240
Db 1117 GCCCATTCAGCTGGCCCTTACTCTGATCTGTTATTTGACTAGGAGGACCGGACCTTGAG 1176

QY 241 GAGCCAAATTAACCTTCGCGCTCCCGAGAACCGCATTTAGTAAGAGAGAAAGATGTGCTGG 300
Db 1177 GAGCCAAATTAACCTTCGCGCTCCCGAGAACCGCATTTAGTAAGAGAGAAAGATGTGCTGG 1236

QY 301 TTCGGCCCACTCTCTCAATGACACTGGCAACTATACCTGATGTTAAGGAACACTACA 360
Db 1237 TTCGGCCCACTCTCTCAATGACACTGGCAACTATACCTGATGTTAAGGAACACTACA 1296

QY 361 TATTGACGAAAGTTCATTTCCCTTGGAAAGTTGTTCAAAAAGACAGCTGTTTCAATCC 420
Db 1297 TATTGACGAAAGTTCATTTCCCTTGGAAAGTTGTTCAAAAAGACAGCTGTTTCAATCC 1356

QY 421 CCATGAAACTCCAGTGCATAACTGTATATAGAAATATGGCAATTCAGAGGATCACTGCT 480
Db 1357 CCATGAAACTCCAGTGCATAACTGTATATAGAAATATGGCAATTCAGAGGATCACTGCT 1416

QY 481 CCAATGTAGATGGATATTTCTTCCAGTGTCAAAACCGACTATCACTTGGTATATGGGC 540
Db 1417 CCAATGTAGATGGATATTTCTTCCAGTGTCAAAACCGACTATCACTTGGTATATGGGC 1476

QY 541 TGTATATAATACGAAATTTTAATATGTAATACCGAGAGGTATGAACTTGATTTCTCTC 600
Db 1477 TGTATATAATACGAAATTTTAATATGTAATACCGAGAGGTATGAACTTGATTTCTCTC 1536

QY 601 ATTGCCTTAATTTCAAAATATGAAATTAACATGTTGTTTACATATCCAGAAATGGA 660
Db 1537 ATTGCCTTAATTTCAAAATATGAAATTAACATGTTGTTTACATATCCAGAAATGGA 1596

QY 661 CGTAGCTTTTCATCTCACAGGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAAAATGCA 720
Db 1597 CGTAGCTTTTCATCTCACAGGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAAAATGCA 1656

QY 721 GTGCCCCCTGTGATCCATTCACCTAATGATCATGTGTTCTATGAGAAAGAACCCAGAGAG 780
Db 1657 GTGCCCCCTGTGATCCATTCACCTAATGATCATGTGTTCTATGAGAAAGAACCCAGAGAG 1716

QY 781 GAGCTACTCATTTCCCTGTACGGTCTATTTTAGTTTCTGATGATTTCTCGCAATGAGTT 840
Db 1717 GAGCTACTCATTTCCCTGTACGGTCTATTTTAGTTTCTGATGATTTCTCGCAATGAGTT 1776

QY 841 TGGTGACCATTTGATGGAAAAAACCCTGATGATCATCACTATTTGATGTGTCAACCAATACGAA 900
Db 1777 TGGTGACCATTTGATGGAAAAAACCCTGATGATCATCACTATTTGATGTGTCAACCAATACGAA 1836

QY 901 AGTATAAGTCATAGTAGACAGAGATGAAACAGAACTCAGATTTTGAGCATCAAGAAA 960
Db 1837 AGTATAAGTCATAGTAGACAGAGATGAAACAGAACTCAGATTTTGAGCATCAAGAAA 1896

QY 961 GTTACTCTGAGGATCTCAAGCGCAGCTATGTCTGTCTGCTAGAAAGTGCACCAAGCGGAA 1020
Db 1897 GTTACTCTGAGGATCTCAAGCGCAGCTATGTCTGTCTGCTAGAAAGTGCACCAAGCGGAA 1956
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QY 1021 GTTGCCAAAGCAGCCCAAGGTGAAGCAGAGAAAGTGCCAGCTCCAAGATACACAGTGGAA 1077
Db 1957 GTTGCCAAAGCAGCCCAAGGTGAAGCAGAGAAAGTGCCAGCTCCAAGATACACAGTGGAA 2013

RESULT 11
US-11-144-987-15
; Sequence 15, Application US/11144987
; Publication No. US20050272655A1
; GENERAL INFORMATION:
; APPLICANT: Mellis, Scott
; APPLICANT: Karow, Margaret
; APPLICANT: Yancopoulos, George
; APPLICANT: Papadopoulos, Joanne
; TITLE OF INVENTION: Methods of Using IL-1 Antagonists to Treat Autoinflammatory Disease
; FILE REFERENCE: REG 2050A
; CURRENT APPLICATION NUMBER: US/11/144,987
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: 60/577,023
; PRIOR FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 2748
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-144-987-15

Query Match      49.2%; Score 1015; DB 7; Length 2748;
Best Local Similarity 100.0%; Pred. No. 4.7e-315;
Matches 1015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 60 CTCAGAACGCTGCGATGACTGGGGACTAGACACCATGAGGCAAAATCCCAAGTGTGTTGAAGA 119
Db 1044 CTCAGAACGCTGCGATGACTGGGGACTAGACACCATGAGGCAAAATCCCAAGTGTGTTGAAGA 1103

QY 120 TGAGCCAGCTCGCATCAAGTGGCCACTCTTTGAACTCTTTGAACTTCAACTACAGCAC 179
Db 1104 TGAGCCAGCTCGCATCAAGTGGCCACTCTTTGAACTCTTTGAACTTCAACTACAGCAC 1163

QY 180 AGCCCATTCAGCTGGCCCTTACTCTGATCTGTTGATGAGTGGAGGACCGGACCTTGA 239
Db 1164 AGCCCATTCAGCTGGCCCTTACTCTGATCTGTTGATGAGTGGAGGACCGGACCTTGA 1223

QY 240 GGAGCCAAATTAACCTTCGCGCTCCCGAGAACCGCATTAAGTAAAGGAGAAAGATGTGCTGTG 299
Db 1224 GGAGCCAAATTAACCTTCGCGCTCCCGAGAACCGCATTAAGTAAAGGAGAAAGATGTGCTGTG 1283

QY 300 GTTCCGGCCCACTCTCTCAATGACACTGGGCAACTATACCTGCTCATGTTAAGGAAACACTAC 359
Db 1284 GTTCCGGCCCACTCTCTCAATGACACTGGGCAACTATACCTGCTCATGTTAAGGAAACACTAC 1343

QY 360 ATATTGACGAGAAAGTTGCTATTTCCCTTGGAAAGTTGTTCAAAAGACAGCTGTTTCAATTC 419
Db 1344 ATATTGACGAGAAAGTTGCTATTTCCCTTGGAAAGTTGTTCAAAAGACAGCTGTTTCAATTC 1403

QY 420 CCCCATGAAACTCCAGTGCATAAACTGTATATAGAAATATGCGATTCAGAGGATCACTTG 479
Db 1404 CCCCATGAAACTCCAGTGCATAAACTGTATATAGAAATATGCGATTCAGAGGATCACTTG 1463

QY 480 TCCAAATGTAGATGATATTTTCTTCCAGTGTCAAACCGACTATCACTTGTGTATATGGG 539
Db 1464 TCCAAATGTAGATGATATTTTCTTCCAGTGTCAAACCGACTATCACTTGTGTATATGGG 1523

QY 540 CTGTTTATAAATACAGAAATTTTAATATGTAATACCCGAGGATGAACTTCAGTTTCTCT 599
Db 1524 CTGTTTATAAATACAGAAATTTTAATATGTAATACCCGAGGATGAACTTCAGTTTCTCT 1583

QY 600 CATTCGCTTAATTTTCAAAATATGGAATTTACACATGTGTGTTACATATCCAGAAAAATCG 659
Db 1584 CATTCGCTTAATTTTCAAAATATGGAATTTACACATGTGTGTTACATATCCAGAAAAATCG 1643

QY 660 AGGTACGTTTCACTCTCACAGGACTCTGACTGTGTAAGGTAGTAGGCTCTCCAAAAAATGCG 719
```

Db 1644 ACCTACGTTTCTCATCTCACCAGGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAAATGC 1703
Qy 720 AGTGCCCGCTGTGATCCATTACCTAATGATCATGTGGTCTATCAGAAAAGAACCCAGGAGA 779
Db 1704 AGTGCCCGCTGTGATCCATTACCTAATGATCATGTGGTCTATCAGAAAAGAACCCAGGAGA 1763
Qy 780 GGAGCTACTCATTCCTGTACGGTCTATTTTGTAGTTTCTGATGGATTCTCGCAATGAGGT 839
Db 1764 GGAGCTACTCATTCCTGTACGGTCTATTTTGTAGTTTCTGATGGATTCTCGCAATGAGGT 1823
Qy 840 TTGGTGGACCATTTGATGGAAAAAACCCTGATGACATCACTATTGATGTCACCAATTAAACGA 899
Db 1824 TTGGTGGACCATTTGATGGAAAAAACCCTGATGACATCACTATTGATGTCACCAATTAAACGA 1883
Qy 900 AAGTATAAGTCATAGTAGACAGAGATGAACAAAGAACTCAGATTTTTGAGCATCAAGAA 959
Db 1884 AAGTATAAGTCATAGTAGACAGAGATGAACAAAGAACTCAGATTTTTGAGCATCAAGAA 1943
Qy 960 AGTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTCATGCTAGAAAGTGCCAAAGCGGA 1019
Db 1944 AGTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTCATGCTAGAAAGTGCCAAAGCGGA 2003
Qy 1020 AGTTGCCAAAGCAGCCAAAGGTGAAGCAGAAAAGTGCCAGCTCCAAGATACACAGTG 1074
Db 2004 AGTTGCCAAAGCAGCCAAAGGTGAAGCAGAAAAGTGCCAGCTCCAAGATACACAGTG 2058

RESULT 12

US-11-144-987-17

; Sequence 17, Application US/11144987

; Publication No. US20050272655A1

; GENERAL INFORMATION:

; APPLICANT: Mellis, Scott

; APPLICANT: Karow, Margaret

; APPLICANT: Yancopoulos, George

; APPLICANT: Papadopoulos, Joanne

; TITLE OF INVENTION: Methods of Using IL-1 Antagonists to Treat Autoinflammatory Disease

; CURRENT APPLICATION NUMBER: US/11/144,987

; CURRENT FILING DATE: 2005-06-03

; PRIOR FILING DATE: 2004-06-04

; NUMBER OF SEQ ID NOS: 26

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 17

; LENGTH: 2754

; TYPE: DNA

; ORGANISM: Homo sapiens

US-11-144-987-17

Query Match

Best Local Similarity 100.0%; Pred. No. 4.7e-315;

Matches 1015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 60 CTCAGAACGCTGCGATGACCTGGGACCTAGACACCATGAGGCAAAATCCAAAGTGTTCGAAGA 119
Db 1044 CTCAGAACGCTGCGATGACCTGGGACCTAGACACCATGAGGCAAAATCCAAAGTGTTCGAAGA 1103
Qy 120 TGAGCCAGCTCGCATCAAGTGCCCACTCTTTTGAACACCTCTTGAATTCAACTACAGCAC 179
Db 1104 TGAGCCAGCTCGCATCAAGTGCCCACTCTTTGAACACCTCTTGAATTCAACTACAGCAC 1163
Qy 180 AGCCATTAGCTGGCCCTTACTCTGATCTGGTATTTGAGCTAGGAGGACCGGACCTTGA 239
Db 1164 AGCCATTAGCTGGCCCTTACTCTGATCTGGTATTTGAGCTAGGAGGACCGGACCTTGA 1223
Qy 240 GGAGCCAAATTAACCTTCGCGCTCCCGAGAACCCGATTTAGTAAAGAGAAAGATGTCTGTG 299
Db 1224 GGAGCCAAATTAACCTTCGCGCTCCCGAGAACCCGATTTAGTAAAGAGAAAGATGTCTGTG 1283
Qy 300 GTTCCGCGCCCACTCTCTCTCAATGACACTGCGCAACTATACCTGCTGTTTAAAGGAACACTAC 359

Query Match		49.2%;	Score 1015;	DB 7;	Length 2754;
Best Local Similarity		100.0%;	Pred. No. 4.7e-315;		
Matches 1015;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	60	CTCAGAACCTCGATGATCTGGGACTAGACACCATGAGGCAAAATCCAAAGTGTGTAAGA	119		
DB	1044	CTCAGAACCTCGATGATCTGGGACTAGACACCATGAGGCAAAATCCAAAGTGTGTAAGA	1103		
QY	120	TGAGCCAGCTCCATCAAGTGCCCACTCTTTGAACACACTTCTTGAATTCACATACAGCAC	179		
DB	1104	TGAGCCAGCTCCATCAAGTGCCCACTCTTTGAACACACTTCTTGAATTCACATACAGCAC	1163		
QY	180	AGCCCATTCAGCTGGCCTTACTCTGATCTGTGATTGGACTAGGACGACCGGACCTTGA	239		
DB	1164	AGCCCATTCAGCTGGCCTTACTCTGATCTGTGATTGGACTAGGACGACCGGACCTTGA	1223		
QY	240	GGAGCCAATTAACTTCGCGCTCCCGAGAACCGCATTTAGTAAGGAGAAAGATGTGCTGTG	299		
DB	1224	GGAGCCAATTAACTTCGCGCTCCCGAGAACCGCATTTAGTAAGGAGAAAGATGTGCTGTG	1283		
QY	300	GTTCCGGCCCACTCTCTCAATGACACTGGCACTATACCTGCATGTTAAGGAACACTAC	359		
DB	1284	GTTCCGGCCCACTCTCTCAATGACACTGGCACTATACCTGCATGTTAAGGAACACTAC	1343		
QY	360	ATATTGCAGCAAGTTGCAATTTCCCTTGGAACTTGTTCAAAAGACAGCTGTTCAATTTC	419		
DB	1344	ATATTGCAGCAAGTTGCAATTTCCCTTGGAACTTGTTCAAAAGACAGCTGTTCAATTTC	1403		
QY	420	CCCATGAAACTCCAGTGATCAATACTGTATATAGAAATGATGATTCAGAGGATCACTTG	479		
DB	1404	CCCATGAAACTCCAGTGATCAATACTGTATATAGAAATGATGATTCAGAGGATCACTTG	1463		
QY	480	TCCAATGATGATGATATTTTCCCTCCAGTGTCAAAACGACTATCACTTGGTATATGG	539		
DB	1464	TCCAATGATGATGATATTTTCCCTCCAGTGTCAAAACGACTATCACTTGGTATATGG	1523		
QY	540	CTGTATTAAAAATACAGAAATTTTAAATGTAATACCCGAAGGTATGAACCTGAGTTTCT	599		
DB	1524	CTGTATTAAAAATACAGAAATTTTAAATGTAATACCCGAAGGTATGAACCTGAGTTTCT	1583		
QY	600	CATTGCTTAATTTCAAATTAATGGAATTPACATGTGTGTTGTAATATCCAGAAATGG	659		
DB	1584	CATTGCTTAATTTCAAATTAATGGAATTPACATGTGTGTTGTAATATCCAGAAATGG	1643		
QY	660	ACGTACGTTTCATCTCACAGGACTCTGACTCTAAAGGTAGTAGGCTCTCCAAAAATGC	719		
DB	1644	ACGTACGTTTCATCTCACAGGACTCTGACTCTAAAGGTAGTAGGCTCTCCAAAAATGC	1703		
QY	720	AGTGCCCTCTGTATCCATTTACCTAAATGATCATGTGTTCTATGAGAAAGAACCCAGGAGA	779		
DB	1704	AGTGCCCTCTGTATCCATTTACCTAAATGATCATGTGTTCTATGAGAAAGAACCCAGGAGA	1763		
QY	780	GGAGTACTCATCTCCCTGACGGTCTATTTTATGTTTCTGATGATTTCTCGCAATGAGT	839		
DB	1764	GGAGTACTCATCTCCCTGACGGTCTATTTTATGTTTCTGATGATTTCTCGCAATGAGT	1823		
QY	840	TTGTGGACCATTTGAGAAAAAACCTGATCACATCACTATTGATGTCACCATTAACGA	899		
DB	1824	TTGTGGACCATTTGAGAAAAAACCTGATCACATCACTATTGATGTCACCATTAACGA	1883		
QY	900	AAATATAAGTCTAGTAGAACAGAAATGAAAAAGAACTCAGATTTTGGAGCATCAAGAA	959		
DB	1884	AAATATAAGTCTAGTAGAACAGAAATGAAAAAGAACTCAGATTTTGGAGCATCAAGAA	1943		
QY	960	AGTTACCTCTGAGGATCTCAAGCGGAGCTATCTGTCTATGCTAGAGTGCCAAAGGCGA	1019		
DB	1944	AGTTACCTCTGAGGATCTCAAGCGGAGCTATCTGTCTATGCTAGAGTGCCAAAGGCGA	2003		
QY	1020	AGTTGCCAAAGCAGCCAGGTGAAAGCAAGTGCAGCTCCAGATACACAGTG	1074		
DB	2004	AGTTGCCAAAGCAGCCAGGTGAAAGCAAGTGCAGCTCCAGATACACAGTG	2058		

RESULT 14					
US-10-750-185-48357/c					
; Sequence 48357, Application US/10750185					
; Publication No. US20050260603A1					
; GENERAL INFORMATION:					
; APPLICANT: MMI GENOMICS, INC.					
; APPLICANT: DENISE, Sue K.					
; APPLICANT: KERR, Richard					
; APPLICANT: ROSENFELD, David					
; APPLICANT: HOLM, Tom					
; APPLICANT: BATES, Stephen					
; APPLICANT: FANTIN, Dennis					
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS					
; FILE REFERENCE: MM1100-2					
; CURRENT APPLICATION NUMBER: US/10/750,185					
; CURRENT FILING DATE: 2003-12-31					
; PRIOR APPLICATION NUMBER: US 60/437,482					
; PRIOR FILING DATE: 2002-12-31					
; NUMBER OF SEQ ID NOS: 64922					
; SOFTWARE: PatentIN version 3.1					
; SEQ ID NO 48357					
; LENGTH: 5178					
; TYPE: DNA					
; ORGANISM: Bovine		19866881094067			
US-10-750-185-48357					
Query Match		5.5%;	Score 114.2;	DB 6;	Length 5178;
Best Local Similarity		84.8%;	Pred. No. 1.6e-25;		
Matches 128;		Conservative 0;	Mismatches 23;	Indels 0;	Gaps 0;
QY	901	AGTAAAGTCATAGTAGAACACAGAACTGAAACCAAGAACTCAGATTTTGAGCATCAAGAA	960		
DB	1423	AGTGAATTTCTAAAGTATACAGACCGACACAGAACTCAGCTTTTGAGCATCAAGAA	1364		
QY	961	GTTACTCTGAGGATCTCAAGCGCAGCTATGTCTGTCTATGCTAGAGTGCCAAAGCGAA	1020		
DB	1363	GTTACTCTGAGGATCTCAAGCGCAATTTATGTCTGTCTATGCTAGAGTGCCAAAGCGGAG	1304		
QY	1021	GTTGCCAAGCAGCCCAAGGTGAAGCAGAAAG	1051		
DB	1303	GTTGACAGCAGCCCAATGTGAACAGAAAG	1273		
RESULT 15					
US-10-750-185-48351/c					
; Sequence 48351, Application US/10750185					
; Publication No. US20050260603A1					
; GENERAL INFORMATION:					
; APPLICANT: MMI GENOMICS, INC.					
; APPLICANT: DENISE, Sue K.					
; APPLICANT: KERR, Richard					
; APPLICANT: ROSENFELD, David					
; APPLICANT: HOLM, Tom					
; APPLICANT: BATES, Stephen					
; APPLICANT: FANTIN, Dennis					
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS					
; FILE REFERENCE: MM1100-2					
; CURRENT APPLICATION NUMBER: US/10/750,185					
; CURRENT FILING DATE: 2003-12-31					
; PRIOR APPLICATION NUMBER: US 60/437,482					
; PRIOR FILING DATE: 2002-12-31					
; NUMBER OF SEQ ID NOS: 64922					
; SOFTWARE: PatentIN version 3.1					
; SEQ ID NO 48351					
; LENGTH: 1388					
; TYPE: DNA					
; ORGANISM: Bovine		19866880606021			
US-10-750-185-48351					
Query Match		2.9%;	Score 60.2;	DB 6;	Length 1388;
Best Local Similarity		78.0%;	Pred. No. 1.4e-08;		
Matches 85;		Conservative 0;	Mismatches 23;	Indels 1;	Gaps 1;

Qy 274 ATTAGTAAGGAGAAAGATGTGCTGTGTTCCGGCCCACTCTC-CTCAATGACACTGGCAA 332
Db |||||
Qy 1388 ATTAGTAAGGAGAAAGACGTGCTCTGTTCCGGCCCACTCTC-CTCAATGACACTGGCAA 1329
Db |||||
Qy 333 CTATACCTGCATGTTAAGGAACACTACATATTGCAGCAAGTTGCATTT 381
Db |||||
Qy 1328 CTATACCTGCATGTTAAGGTAGGCTGACGCTTGTGTGTTCTTTCCCTTT 1280
Db |||||

Search completed: December 14, 2005, 15:33:58
Job time : 264 secs

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OM protein - protein search, using sw model

Run on: December 7, 2005, 13:33:46 ; Search time 167 Seconds
(without alignments)
1718.855 Million cell updates/sec

Title: US-10-061-727-2
Perfect score: 3669
Sequence: 1 MTLWCVVSLFYFYGILQSDA.....SALALHFTDLNNDFYIL 687

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pcp.*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pcp.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pcp.*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pcp.*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pcp.*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3667	99.9	687	4	US-10-061-727-2 Sequence 2, Appli
2	3281	89.4	685	4	US-10-061-727-4 Sequence 4, Appli
3	2595	70.7	822	4	US-10-167-127-16 Sequence 16, Appli
4	2586	70.5	570	4	US-10-011-548-36 Sequence 36, Appli
5	2586	70.5	570	4	US-10-167-127-10 Sequence 10, Appli
6	2580	70.3	570	4	US-10-215-211-4 Sequence 4, Appli
7	2327.5	63.4	570	4	US-10-011-548-21 Sequence 21, Appli
8	2327.5	63.4	570	4	US-10-205-219-23 Sequence 23, Appli
9	1937.5	52.8	915	4	US-10-282-162-52 Sequence 52, Appli
10	1937.5	52.8	915	5	US-10-840-138-22 Sequence 22, Appli
11	1937.5	52.8	915	5	US-10-945-068-22 Sequence 22, Appli
12	1937.5	52.8	915	6	US-11-056-730-22 Sequence 22, Appli
13	1937.5	52.8	915	6	US-11-134-114-52 Sequence 52, Appli
14	1937.5	52.8	917	4	US-10-282-162-54 Sequence 54, Appli
15	1937.5	52.8	917	4	US-10-282-162-56 Sequence 56, Appli
16	1937.5	52.8	917	5	US-10-840-138-24 Sequence 24, Appli
17	1937.5	52.8	917	5	US-10-840-138-26 Sequence 26, Appli
18	1937.5	52.8	917	5	US-10-945-068-24 Sequence 24, Appli
19	1937.5	52.8	917	6	US-10-945-068-26 Sequence 26, Appli
20	1937.5	52.8	917	6	US-11-056-730-24 Sequence 24, Appli
21	1937.5	52.8	917	6	US-11-056-730-26 Sequence 26, Appli
22	1937.5	52.8	917	6	US-11-134-114-54 Sequence 54, Appli
23	1937.5	52.8	917	6	US-11-134-114-56 Sequence 56, Appli
24	1935	52.7	359	6	US-11-096-039-4 Sequence 4, Appli
25	1935	52.7	900	4	US-10-282-162-40 Sequence 40, Appli
26	1935	52.7	900	5	US-10-840-138-10 Sequence 10, Appli
27	1935	52.7	900	5	US-10-945-068-10 Sequence 10, Appli

28	1935	52.7	900	6	US-11-056-730-10	Sequence 10, Appli
29	1935	52.7	900	6	US-11-134-114-40	Sequence 40, Appli
30	1935	52.7	902	4	US-10-282-162-42	Sequence 42, Appli
31	1935	52.7	902	4	US-10-282-162-44	Sequence 44, Appli
32	1935	52.7	902	5	US-10-840-138-12	Sequence 12, Appli
33	1935	52.7	902	5	US-10-840-138-14	Sequence 14, Appli
34	1935	52.7	902	5	US-10-945-068-12	Sequence 12, Appli
35	1935	52.7	902	5	US-10-945-068-14	Sequence 14, Appli
36	1935	52.7	902	6	US-11-056-730-12	Sequence 12, Appli
37	1935	52.7	902	6	US-11-056-730-14	Sequence 14, Appli
38	1935	52.7	902	6	US-11-134-114-42	Sequence 42, Appli
39	1935	52.7	902	6	US-11-134-114-44	Sequence 44, Appli
40	1934	52.7	359	4	US-10-215-211-6	Sequence 6, Appli
41	1930	52.6	910	3	US-09-313-942-28	Sequence 28, Appli
42	1930	52.6	910	3	US-09-935-868-28	Sequence 28, Appli
43	1930	52.6	910	4	US-10-287-035-28	Sequence 28, Appli
44	1930	52.6	910	4	US-10-282-162-28	Sequence 28, Appli
45	1930	52.6	910	5	US-10-840-138-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-10-061-727-2
; Sequence 2, Application US/10061727
; Publication No. US20030170632A1
; GENERAL INFORMATION:
; APPLICANT: Sims, John E.
; TITLE OF INVENTION: IL-1 RECEPTOR ACCESSORY PROTEIN
; FILE REFERENCE: 3151-A
; CURRENT APPLICATION NUMBER: US/10/061,727
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: US 60/244,831
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 687
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (598)-(598)
; OTHER INFORMATION: The 'Xaa' at location 598 stands for Thr or Pro.
US-10-061-727-2

Query Match	99.9%	Score 3667;	DB 4;	Length 687;
Best Local Similarity	100.0%;	Pred. No. 2e-311;		
Matches 687;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MTLWCVVSLFYFYGILQSDASERCDWGLDMRQIQVPEDEPARIKCPLFHFHLPKFNYST	60	
Db	1	MTLWCVVSLFYFYGILQSDASERCDWGLDMRQIQVPEDEPARIKCPLFHFHLPKFNYST	60	
Qy	61	AHSAGTLIYWTQRDRDLPEINFRIPENRISKEKVLWFRPTLLNDGNTGNTCLRNNT	120	
Db	61	AHSAGTLIYWTQRDRDLPEINFRIPENRISKEKVLWFRPTLLNDGNTGNTCLRNNT	120	
Qy	121	YCSKVAFLVQKDSFNSPKMLPVHKLIEYGIQRTICPNVDGYFPSSVKPTITWYMG	180	
Db	121	YCSKVAFLVQKDSFNSPKMLPVHKLIEYGIQRTICPNVDGYFPSSVKPTITWYMG	180	
Qy	181	CYKIQNFNNVPEGMNLSFLIALISNNNGYTCVVYTPENGRTFHLTRTLTKVVGSPKNA	240	
Db	181	CYKIQNFNNVPEGMNLSFLIALISNNNGYTCVVYTPENGRTFHLTRTLTKVVGSPKNA	240	
Qy	241	VPVPHSPNDHVYKEKGEELLIPCTVYFSLMDSRNEVWMTIDGKPPDDITIDVTINE	300	
Db	241	VPVPHSPNDHVYKEKGEELLIPCTVYFSLMDSRNEVWMTIDGKPPDDITIDVTINE	300	
Qy	301	SISHSRTEDETRTQILSIKKVTSBDLKRYSVCHARSASAKGEVAKAKVKQKVPAPRYTVEL	360	

Db 301 SISHRTDETRTQILSIKKVTSSEDLKRSVYCHARSAGKGEVAKAAKVKQVPAPRYTVEL 360
Qy 361 ACAGFATVLLVILIVVYHVWLEWLVFYRAHFGTDETLIDGKEYDIYVSVARNAREEEF 420
Db 361 ACAGFATVLLVILIVVYHVWLEWLVFYRAHFGTDETLIDGKEYDIYVSVARNAREEEF 420
Qy 421 VLLTLRGVLENEFGYKLCIFDRDSLPGGNTVEAFDFIORSRRMIVVLSPDYVTEKISM 480
Db 421 VLLTLRGVLENEFGYKLCIFDRDSLPGGNTVEAFDFIORSRRMIVVLSPDYVTEKISM 480
Qy 481 LEFKLGVMCQNSIATKLIIVVEYRPLEHPHPGILQLKESVSVSWKGEKSKHSGSKFWKAL 540
Db 481 LEFKLGVMCQNSIATKLIIVVEYRPLEHPHPGILQLKESVSVSWKGEKSKHSGSKFWKAL 540
Qy 541 RLALPLRSLSSASSGWNESCSCSSQSDISLDHVORRRSRRLKEPPELOSSERAAGSPAPCXMS 600
Db 541 RLALPLRSLSSASSGWNESCSCSSQSDISLDHVORRRSRRLKEPPELOSSERAAGSPAPCXMS 600
Qy 601 KHRGKSATRCCTVYCEGENHLRNKSRABEIHNPQWETHLCKPVPQSESTQWIONGTRL 660
Db 601 KHRGKSATRCCTVYCEGENHLRNKSRABEIHNPQWETHLCKPVPQSESTQWIONGTRL 660
Qy 661 EPPAPQISALALHHFTDLSNNNDFYIL 687
Db 661 EPPAPQISALALHHFTDLSNNNDFYIL 687

RESULT 2
US-10-061-727-4
; Sequence 4, Application US/10061727
; Publication No. US20030170632A1
; GENERAL INFORMATION:
; APPLICANT: Sims, John E.
; APPLICANT: Smith, John E.
; TITLE OF INVENTION: IL-1 RECEPTOR ACCESSORY PROTEIN
; FILE REFERENCE: 3151-A
; CURRENT APPLICATION NUMBER: US/10/061,727
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: US 60/244,831
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 685
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-061-727-4

Query Match 89.4%; Score 3281; DB 4; Length 685;
Best Local Similarity 88.5%; Pred. No. 1.2e-277;
Matches 608; Conservative 39; Mismatches 38; Indels 2; Gaps 2;
Qy 1 MTLWCVSLYFYGILOSASERCDDWGLDMRQIQVFEDEPARIKCPLFEHLKFNYSY 60
Db 1 MGLLWYLSUSFYGILOSASERCDDWGLDMRQIQVFEDEPARIKCPLFEHLKFNYSY 60
Qy 61 AHSAGLTLIWYTRQDRDLDEEPINFRLENRISEKEDVLMFRPTLLNDTGNVTCMLRNTT 120
Db 61 AHSAGLTLIWYTRQDRDLDEEPINFRLENRISEKEDVLMFRPTLLNDTGNVTCMLRNTT 120
Qy 121 YCSKVAAPLEVVQKDSFCNFSMKLPVHKLYIEYGIQRIITCPNVVDGYFPSSVKPTIYWYG 180
Db 121 YCSKVAAPLEVVQKDSFCNFSMKLPVHKLYIEYGIQRIITCPNVVDGYFPSSVKPTIYWYG 180
Qy 181 CYKIQNFNNVPEGMNLSFLIALISNNGNYTCVVYPENGRTPHLTRTLTKVVGSPKNA 240
Db 181 CTEIVDPHNLVPEGMNLSFLIALISNNGNYTCVVYPENGRTPHLTRTLTKVVGSPKNA 240
Qy 241 VPPVIHSPNDHVYVEKEPGEELIIPCTVYFSFLMDSRNEVWWTIDGKKPDDITDVTINE 300
Db 241 LPQIYSPNDHVYVEKEPGEELIIPCTVYFSFLMDSRNEVWWTIDGKKPDDITDVTINE 300

Qy 301 SISHRTDETRTQILSIKKVTSSEDLKRSVYCHARSAGKGEVAKAAKVKQVPAPRYTVEL 360
Db 301 SVSYSTDETRTQILSIKKVTSSEDLKRSVYCHARNYVCHARTKGEAQAAKVKQVIPPRYTVEL 360
Qy 361 ACAGFATVLLVILIVVYHVWLEWLVFYRAHFGTDETLIDGKEYDIYVSVARNAREEEF 420
Db 361 ACAGFATVLLVILIVVYHVWLEWLVFYRAHFGTDETLIDGKEYDIYVSVARNAREEEF 420
Qy 421 VLLTLRGVLENEFGYKLCIFDRDSLPGGNTVEAFDFIORSRRMIVVLSPDYVTEKISM 480
Db 421 VLLTLRGVLENEFGYKLCIFDRDSLPGGNTVEAFDFIORSRRMIVVLSPDYVTEKISM 480
Qy 481 LEFKLGVMCQNSIATKLIIVVEYRPLEHPHPGILQLKESVSVSWKGEKSKHSGSKFWKAL 540
Db 481 LEFKLGVMCQNSIATKLIIVVEYRPLEHPHPGILQLKESVSVSWKGEKSKHSGSKFWKAL 540
Qy 541 RLALPLRSLSSASSGWNESCSCSSQSDISLDHVORRRSRRLKEPPELOSSERAAGSPAPCXMS 600
Db 541 RLALPLRSLSSASSGWNESCSCSSQSDISLDHVQ-RRSRLKEPPELRSRVSERGAEPAGTMS 599
Qy 601 KHRGKSATRCCTVYCEGENHLRNKSRABEIHNPQWETHLCKPVPQSESTQWIONGTRL 660
Db 600 KHRGKPSAACRCCTVYCEGESHLRSKRAEMTHPQWETHLCKPPLQESSESQWIONGTRP 659
Qy 661 EPPAPQISALALHHFTDLSNNNDFYIL 687
Db 660 E-PAPQISALALRHFTDLSNNNDFYIL 685

RESULT 3
US-10-167-127-16
; Sequence 16, Application US/10167127
; Publication No. US20030100031A1
; GENERAL INFORMATION:
; APPLICANT: DOWER, STEVEN
; APPLICANT: DUFF, GORDON W.
; TITLE OF INVENTION: INTEGRATIVE ASSAYS FOR MONITORING MOLECULAR ASSEMBLY
; FILE REFERENCE: MSA-026.01 (20974-2601)
; CURRENT APPLICATION NUMBER: US/10/167,127
; CURRENT FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: 60/297,305
; PRIOR FILING DATE: 2001-06-11
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 822
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-167-127-16

Query Match 70.7%; Score 2595; DB 4; Length 822;
Best Local Similarity 82.1%; Pred. No. 1.7e-217;
Matches 499; Conservative 36; Mismatches 45; Indels 28; Gaps 7;
Qy 1 MTLWCVSLYFYGILOSASERCDDWGLDMRQIQVFEDEPARIKCPLFEHLKFNYSY 60
Db 1 MTLWCVSLYFYGILOSASERCDDWGLDMRQIQVFEDEPARIKCPLFEHLKFNYSY 60
Qy 61 AHSAGLTLIWYTRQDRDLDEEPINFRLENRISEKEDVLMFRPTLLNDTGNVTCMLRNTT 120
Db 61 AHSAGLTLIWYTRQDRDLDEEPINFRLENRISEKEDVLMFRPTLLNDTGNVTCMLRNTT 120
Qy 121 YCSKVAAPLEVVQKDSFCNFSMKLPVHKLYIEYGIQRIITCPNVVDGYFPSSVKPTIYWYG 180
Db 121 YCSKVAAPLEVVQKDSFCNFSMKLPVHKLYIEYGIQRIITCPNVVDGYFPSSVKPTIYWYG 180
Qy 181 CYKIQNFNNVPEGMNLSFLIALISNNGNYTCVVYPENGRTPHLTRTLTKVVGSPKNA 240
Db 181 CYKIQNFNNVPEGMNLSFLIALISNNGNYTCVVYPENGRTPHLTRTLTKVVGSPKNA 240
Qy 241 VPPVIHSPNDHVYVEKEPGEELIIPCTVYFSFLMDSRNEVWWTIDGKKPDDITDVTINE 300
Db 241 VPPVIHSPNDHVYVEKEPGEELIIPCTVYFSFLMDSRNEVWWTIDGKKPDDITDVTINE 300

Db 241 VPPVHSPNDHVYVEKEPGEELLIPCTVYFSLMDSRNEVWMTIDGKPPDDITIDVTINE 300
Qy 301 SISHSRTEDETRTQILSIKKVTSSEDLKRSVCHARSAGEVAKAQKVPAPRYTVEL 360
Db 301 SISHSRTEDETRTQILSIKKVTSSEDLKRSVCHARSAGEVAKAQKVPAPRYTVEL 360
Qy 361 ACGFATVLLVILVYVHVYVLEWVLFYRAHFGTDTETILDGKEYDIYVSYARNAEEBEF 420
Db 361 ACGFATVLLVILVYVHVYVLEWVLFYRAHFGTDTETILDGKEYDIYVSYARNAEEBEF 420
Qy 421 VLLTLRGVLENEGYKLCIFDRDSLPGGNTVAVDFIORSRMIIVLSPDYVTEKSI SM 480
Db 421 VLLTLRGVLENEGYKLCIFDRDSLPGGNTVAVDFIORSRMIIVLSPDYVTEKSI SM 480
Qy 481 LEFKLGVMCQNSIATK---LIVVEYRPLEHPHPIQLKES---VSFVSWKGEKSKHG 533
Db 481 LELKAGL---ENMASRGNINVLVQYKAVKETK---VKELKRAKTVLTVIKWGEKSKYPQ 535
Qy 534 SKFWKALRLALPURLSASSGNWESSQSODISLDHVQRRRLKEPPELQSSERAAGSP 593
Db 536 GRFWKQLQVAMPVKKSPRESSSDEQGLSYS--SLKNVGR-----VPP-----ARDP 579
Qy 594 PAPGWSK 601
Db 580 PVATWVSK 587

RESULT 4

US-10-011-548-36
; Sequence 36, Application US/10011548
; Publication No. US20030055218A1
; GENERAL INFORMATION:
; APPLICANT: Timans, Jacqueline C.
; Debets, Johannes Eduard Maria
; Antonius
; Sana, Theodore R.
; Bazan, J. Fernando
; Kastelein, Robert A.
; TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and
; Methods
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/011,548
; FILING DATE: 22-Oct-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/173,151
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 60/065,776
; FILING DATE: 17-NOV-1997
; APPLICATION NUMBER: US 60/078,008
; FILING DATE: 12-MAR-1998
; APPLICATION NUMBER: US 60/081,883
; FILING DATE: 15-APR-1998
; APPLICATION NUMBER: US 60/095,997
; FILING DATE: 10-AUG-1998
; APPLICATION NUMBER: US 60/078,416
; FILING DATE: 18-MAR-1998
; APPLICATION NUMBER: US 60/062,066
; FILING DATE: 15-OCT-1997
; ATTORNEY/AGENT INFORMATION:

NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0767X
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
TELEFAX: (650)496-1200
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 570 amino acids
TYPE: amino acid
STRANDEDNESS: No. US20030055218A1 Relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-10-011-548-36
Query Match 70.5%; Score 2586; DB 4; Length 570;
Best Local Similarity 85.3%; Pred. No. 6.1e-217;
Matches 488; Conservative 35; Mismatches 37; Indels 12; Gaps 4;
Qy 1 MTLWCVVSLYFYGILQSDASERCDDWGLDMRQIQVFEDEPARIKCPLFEHFLKFNYST 60
Db 1 MTLWCVVSLYFYGILQSDASERCDDWGLDMRQIQVFEDEPARIKCPLFEHFLKFNYST 60
Qy 61 AHSAGLTLLIYWWTQRDLBEPINFRLPENRISKEKVLWFRPTLLNDTGNVTCMLRNTT 120
Db 61 AHSAGLTLLIYWWTQRDLBEPINFRLPENRISKEKVLWFRPTLLNDTGNVTCMLRNTT 120
Qy 121 YCSKVAPELVVQKDSFCNSPMKLPVHKLYIEYGIQRITCPNVGDFPSSVKPTITWYMG 180
Db 121 YCSKVAPELVVQKDSFCNSPMKLPVHKLYIEYGIQRITCPNVGDFPSSVKPTITWYMG 180
Qy 181 CYKIQNFNNVPEGMNLSFLIALISNNGNYTCVVTYPENGRTPHLTRTLTVKVVGSPKNA 240
Db 181 CYKIQNFNNVPEGMNLSFLIALISNNGNYTCVVTYPENGRTPHLTRTLTVKVVGSPKNA 240
Qy 241 VPPVHSPNDHVYVEKEPGEELLIPCTVYFSLMDSRNEVWMTIDGKPPDDITIDVTINE 300
Db 241 VPPVHSPNDHVYVEKEPGEELLIPCTVYFSLMDSRNEVWMTIDGKPPDDITIDVTINE 300
Qy 301 SISHSRTEDETRTQILSIKKVTSSEDLKRSVCHARSAGEVAKAQKVPAPRYTVEL 360
Db 301 SISHSRTEDETRTQILSIKKVTSSEDLKRSVCHARSAGEVAKAQKVPAPRYTVEL 360
Qy 361 ACGFATVLLVILVYVHVYVLEWVLFYRAHFGTDTETILDGKEYDIYVSYARNAEEBEF 420
Db 361 ACGFATVLLVILVYVHVYVLEWVLFYRAHFGTDTETILDGKEYDIYVSYARNAEEBEF 420
Qy 421 VLLTLRGVLENEGYKLCIFDRDSLPGGNTVAVDFIORSRMIIVLSPDYVTEKSI SM 480
Db 421 VLLTLRGVLENEGYKLCIFDRDSLPGGNTVAVDFIORSRMIIVLSPDYVTEKSI SM 480
Qy 481 LEFKLGVMCQNSIATK---LIVVEYRPLEHPHPIQLKES---VSFVSWKGEKSKHG 533
Db 481 LELKAGL---ENMASRGNINVLVQYKAVKETK---VKELKRAKTVLTVIKWGEKSKYPQ 535
Qy 534 SKFWKALRLALPURLSASSGNWESSQSODI 565
Db 536 GRFWKQLQVAMPVKKSPRESSSDEQGLSYS 567
RESULT 5
US-10-167-127-10
; Sequence 10, Application US/10167127
; Publication No. US20030100031A1
; GENERAL INFORMATION:
; APPLICANT: DOWE, STEVEN
; APPLICANT: DUFF, GORDON W.
; TITLE OF INVENTION: INTEGRATIVE ASSAYS FOR MONITORING MOLECULAR ASSEMBLY
; TITLE OF INVENTION: EVENTS
; FILE REFERENCE: MSA-026.01 (20974-2601)
; CURRENT APPLICATION NUMBER: US/10/167,127
; CURRENT FILING DATE: 2002-06-11

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; PRIOR APPLICATION NUMBER: 60/297,305
; PRIOR FILING DATE: 2001-06-11
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 570
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-167-127-10

Query Match          70.5%; Score 2586; DB 4; Length 570;
Best Local Similarity 85.3%; Pred. No. 6.1e-217;
Matches 488; Conservative 35; Mismatches 37; Indels 12; Gaps 4;

Qy 1 MTLWCVVSLYFYGILQSDASERCDDWGLDMRQIQVFEDEPARIKCPLEFHFLEKFNYST 60
Db 1 MTLWCVVSLYFYGILQSDASERCDDWGLDMRQIQVFEDEPARIKCPLEFHFLEKFNYST 60

Qy 61 AHSAGLTLIYWTRQDRDLLEPINFRLPENRISKEKDVLMFRPTLLNDTGNITCMLRNTT 120
Db 61 AHSAGLTLIYWTRQDRDLLEPINFRLPENRISKEKDVLMFRPTLLNDTGNITCMLRNTT 120

Qy 121 YCSKVAFLVQKDSFCNSPMKLPVHKLYIEYGIQRIITCENVVDGYPSSVKPTITWYMG 180
Db 121 YCSKVAFLVQKDSFCNSPMKLPVHKLYIEYGIQRIITCENVVDGYPSSVKPTITWYMG 180

Qy 181 CYKIQNFNNVIPEGNNLSFLIALISNNGNVTCTVVTYPENGRTPHLTRTLTKVVGSPKNA 240
Db 181 CYKIQNFNNVIPEGNNLSFLIALISNNGNVTCTVVTYPENGRTPHLTRTLTKVVGSPKNA 240

Qy 241 VPPVIHSPNDHVYKEPGEELLIPCTVYFSLMDSRNEVWTTIDGKKPDDITIDVTINE 300
Db 241 VPPVIHSPNDHVYKEPGEELLIPCTVYFSLMDSRNEVWTTIDGKKPDDITIDVTINE 300

Qy 301 SISHSRTEDETRTQILSIKKVTSDELKRSVYCHARSAGVAKAAVKQKVPAPRYTVEL 360
Db 301 SISHSRTEDETRTQILSIKKVTSDELKRSVYCHARSAGVAKAAVKQKVPAPRYTVEL 360

Qy 361 ACGFATVLLVILVYVHYVWLEMLFYRAHFGTDETLIDGKEYDIYVSYARNAEDEEF 420
Db 361 ACGFATVLLVILVYVHYVWLEMLFYRAHFGTDETLIDGKEYDIYVSYARNAEDEEF 420

Qy 421 VLLTLRGVLENEFGYKLCIFDRSLPGCNTVEAFDFIQRSMRMIIVLSYDYVTEKISM 480
Db 421 VLLTLRGVLENEFGYKLCIFDRSLPGGIVTDETLFSFIQSRRLVLSYVYLQGTQAL 480

Qy 481 LEFKLGVMQNSIATK---LIVVEYRPLEHPHPGILQLKES---VSFVSWKGEKSKHSG 533
Db 481 LEFKAGL---ENNASRGNINVLVOYKAVKETK--VKELKRAKTVLTIVIKWGEKSKYPQ 535

Qy 534 SKFWKALRLALPLRSLSASSGWNESCSSQSDI 565
Db 536 GREWQQLQVAMPVKSPRRSSDEQGLSYSSL 567

RESULT 6
US-10-215-211-4
; Sequence 4, Application US/10215211
; Publication No. US20030049255A1
; GENERAL INFORMATION:
; APPLICANT: Sims, John E.
; APPLICANT: Smith, Dirk E.
; TITLE OF INVENTION: INTERLEUKIN-1 RECEPTORS IN THE TREATMENT OF DISEASES
; FILE REFERENCE: 3321-A
; CURRENT APPLICATION NUMBER: US/10/215,211
; CURRENT FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: US 60/310,789
; PRIOR FILING DATE: 2001-08-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 570
; TYPE: PRT

; ORGANISM: Homo sapiens
; US-10-215-211-4

Query Match          70.3%; Score 2580; DB 4; Length 570;
Best Local Similarity 85.6%; Pred. No. 2.1e-216;
Matches 487; Conservative 31; Mismatches 45; Indels 6; Gaps 3;

Qy 1 MTLWCVVSLYFYGILQSDASERCDDWGLDMRQIQVFEDEPARIKCPLEFHFLEKFNYST 60
Db 1 MTLWCVVSLYFYGILQSDASERCDDWGLDMRQIQVFEDEPARIKCPLEFHFLEKFNYST 60

Qy 61 AHSAGLTLIYWTRQDRDLLEPINFRLPENRISKEKDVLMFRPTLLNDTGNITCMLRNTT 120
Db 61 AHSAGLTLIYWTRQDRDLLEPINFRLPENRISKEKDVLMFRPTLLNDTGNITCMLRNTT 120

Qy 121 YCSKVAFLVQKDSFCNSPMKLPVHKLYIEYGIQRIITCENVVDGYPSSVKPTITWYMG 180
Db 121 YCSKVAFLVQKDSFCNSPMKLPVHKLYIEYGIQRIITCENVVDGYPSSVKPTITWYMG 180

Qy 181 CYKIQNFNNVIPEGNNLSFLIALISNNGNVTCTVVTYPENGRTPHLTRTLTKVVGSPKNA 240
Db 181 CYKIQNFNNVIPEGNNLSFLIALISNNGNVTCTVVTYPENGRTPHLTRTLTKVVGSPKNA 240

Qy 241 VPPVIHSPNDHVYKEPGEELLIPCTVYFSLMDSRNEVWTTIDGKKPDDITIDVTINE 300
Db 241 VPPVIHSPNDHVYKEPGEELLIPCTVYFSLMDSRNEVWTTIDGKKPDDITIDVTINE 300

Qy 301 SISHSRTEDETRTQILSIKKVTSDELKRSVYCHARSAGVAKAAVKQKVPAPRYTVEL 360
Db 301 SISHSRTEDETRTQILSIKKVTSDELKRSVYCHARSAGVAKAAVKQKVPAPRYTVEL 360

Qy 361 ACGFATVLLVILVYVHYVWLEMLFYRAHFGTDETLIDGKEYDIYVSYARNAEDEEF 420
Db 361 ACGFATVLLVILVYVHYVWLEMLFYRAHFGTDETLIDGKEYDIYVSYARNAEDEEF 420

Qy 421 VLLTLRGVLENEFGYKLCIFDRSLPGCNTVEAFDFIQRSMRMIIVLSYDYVTEKISM 480
Db 421 VLLTLRGVLENEFGYKLCIFDRSLPGGIVTDETLFSFIQSRRLVLSYVYLQGTQAL 480

Qy 481 LEFKLGVMQNSIATK---LIVVEYRPLEHPHPGILQLKES---VSFVSWKGEKSKHSGSKP 536
Db 481 LEFKAGL---ENNASRGNINVLVOYKAVKETK--VKELKRAKTVLTIVIKWGEKSKYPOGRP 538

Qy 537 WKALRLALPLRSLSASSGWNESCSSQSDI 565
Db 539 WKQLQVAMPVKSPRRSSDEQGLSYSSL 567

RESULT 7
US-10-011-548-21
; Sequence 21, Application US/10011548
; Publication No. US20030055218A1
; GENERAL INFORMATION:
; APPLICANT: Timans, Jacqueline C.
; Debets, Johannes Eduard Maria
; Antonius
; Sana, Theodore R.
; Bazan, J. Fernando
; Kastelein, Robert A.
; TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and
; Methods
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/011,548
FILING DATE: 22-Oct-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/173,151
FILING DATE: <Unknown>
APPLICATION NUMBER: US 60/065,776
FILING DATE: 17-Nov-1997
APPLICATION NUMBER: US 60/078,008
FILING DATE: 12-Mar-1998
APPLICATION NUMBER: US 60/081,883
FILING DATE: 15-Apr-1998
APPLICATION NUMBER: US 60/095,987
FILING DATE: 10-Aug-1998
APPLICATION NUMBER: US 60/078,416
FILING DATE: 18-Mar-1998
APPLICATION NUMBER: US 60/062,066
FILING DATE: 15-Oct-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0767X
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
TELEFAX: (650)496-1200
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 570 amino acids
TYPE: amino acid
STRANDEDNESS: No. US20030055218A1 Relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-10-011-548-21

Query Match 63.4%; Score 2327.5; DB 4; Length 570;
Best Local Similarity 75.9%; Pred. No. 2.6e-194;
Matches 429; Conservative 66; Mismatches 55; Indels 15; Gaps 5;
QY 1 MTLWCVVSLFYGILOSDASERCDDWGLDMRQIQVFEDEPARIKCPLFEHFLKFNYST 60
DB 1 MGLLWYLSLFSYGILOSHASERCDDWGLDMRQIQVFEDEPARIKCPLFEHFLKFNYST 60
QY 61 AHSAGLTLIWYTRQDRDLEBPINFRLPENRISKEKDVLFWRPRLTLLNDTGYTCLMRNTT 120
DB 61 AHSAGLTLIWYTRQDRDLEBPINFRLPENRISKEKDVLFWRPRLTLLNDTGYTCLMRNTT 120
QY 121 YCSKVAFFLEVQKDSFCNSPMKLPVHKLYIEYGIQRTCPNVGYPFSSVKPTITWTMG 180
DB 121 YCSKVAFFLEVQKDSFCNSAMRFPVHKYIEHGHKITCPNVGYPFSSVKPSVTWYKG 180
QY 181 CYKIQNFNNVPIPEGMNLSPFLIALISNNGNYTCVVTYPENGRTPHLTRTLTKVVGSPKNA 240
DB 181 CTEIVDFHNLVPEGMNLSPFLVLSNNGNYTCVVTYPENGRFLHLTRTVTKVVGSPKDA 240
QY 241 VPPVHSPNDHVYKEPGEELLIPCTVYFSLMDSRNEVWMTIDGKKPDDITDVTINE 300
DB 241 LPQIYSNDRVYKEPGEELVIPCXYFSPFIMDSHNEVWMTIDGKKPDDVTDVTINE 300
QY 301 SISHSRTEDETRTQILSIKKVTSDELKRSYVCHARSAGKAEVAKKQKVPAPRYTVEL 360
DB 301 SVSYSSSTEDETRTQILSIKKVTPEDLRNRYVCHARNTKGEAEQAQKQKVPAPRYTVEL 360
QY 361 ACGFATVLLVVLIVVYVHYVWLEMLVYFRAHFGTDETLIDGKEYDIYVSVARNABEEEF 420
DB 361 ACGFATVLLVVLIVVYVHYVWLEMLVYFRAHFGTDETLIDGKEYDIYVSVARNABEEEF 420
QY 421 VLLTLRGVLENEFGYKLCIFDRDLSLPGCNTVEAFDFIQRSRMIVLSPDYVTEKSIISM 480
DB 421 VLLTLRGVLENEFGYKLCIFDRDLSLPGGIVTDETLISFIQKSRRLVLSNPNYLQGTQAL 480
QY 481 LEFKLGVMCNSIATK---LIVVEYRPLEHPHGIQLQKES---VSFVSWKGEKSHSG 533
DB 481 LEFKLGVMCNSIATK---LIVVEYRPLEHPHGIQLQKES---VSFVSWKGEKSHSG 533

QY 481 LEFKLGVMCNSIATK---LIVVEYRPLEHPHGIQLQKES---VSFVSWKGEKSHSG 533
DB 481 LELKAGL---ENMASRGNINVLQYKAVKDMK--VKELKRAKTVLTIVIKWGEKSKYPQ 535
QY 534 SKFWKALRLALPLRSLSSASSGWNES 558
DB 536 GRFWKQLQVAMPVKK---SPRWSSN 557
RESULT 8
US-10-205-219-23
Sequence 23, Application US/10205219
Publication No. US20030138803A1
GENERAL INFORMATION:
APPLICANT: Warner-Lambert Company
APPLICANT: Lee, Kevin
APPLICANT: Dixon, Alistair
APPLICANT: Brookabank, Robert
APPLICANT: Pinnock, Robert
TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
FILE REFERENCE: WL-A-018200
CURRENT APPLICATION NUMBER: US/10/205,219
CURRENT FILING DATE: 2002-07-24
PRIOR APPLICATION NUMBER: GB 0118354.0
PRIOR FILING DATE: 2001-07-27
NUMBER OF SEQ ID NOS: 197
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 23
LENGTH: 570
TYPE: PRT
ORGANISM: Mus musculus
FEATURE:
OTHER INFORMATION: Second subunit of the interleukin 1 receptor complex
US-10-205-219-23

Query Match 63.4%; Score 2327.5; DB 4; Length 570;
Best Local Similarity 75.9%; Pred. No. 2.6e-194;
Matches 429; Conservative 66; Mismatches 55; Indels 15; Gaps 5;
QY 1 MTLWCVVSLFYGILOSDASERCDDWGLDMRQIQVFEDEPARIKCPLFEHFLKFNYST 60
DB 1 MGLLWYLSLFSYGILOSHASERCDDWGLDMRQIQVFEDEPARIKCPLFEHFLKFNYST 60
QY 61 AHSAGLTLIWYTRQDRDLEBPINFRLPENRISKEKDVLFWRPRLTLLNDTGYTCLMRNTT 120
DB 61 AHSAGLTLIWYTRQDRDLEBPINFRLPENRISKEKDVLFWRPRLTLLNDTGYTCLMRNTT 120
QY 121 YCSKVAFFLEVQKDSFCNSPMKLPVHKLYIEYGIQRTCPNVGYPFSSVKPTITWTMG 180
DB 121 YCSKVAFFLEVQKDSFCNSAMRFPVHKYIEHGHKITCPNVGYPFSSVKPSVTWYKG 180
QY 181 CYKIQNFNNVPIPEGMNLSPFLIALISNNGNYTCVVTYPENGRTPHLTRTLTKVVGSPKNA 240
DB 181 CTEIVDFHNLVPEGMNLSPFLVLSNNGNYTCVVTYPENGRFLHLTRTVTKVVGSPKDA 240
QY 241 VPPVHSPNDHVYKEPGEELLIPCTVYFSLMDSRNEVWMTIDGKKPDDITDVTINE 300
DB 241 LPQIYSNDRVYKEPGEELVIPCXYFSPFIMDSHNEVWMTIDGKKPDDVTDVTINE 300
QY 301 SISHSRTEDETRTQILSIKKVTSDELKRSYVCHARSAGKAEVAKKQKVPAPRYTVEL 360
DB 301 SVSYSSSTEDETRTQILSIKKVTPEDLRNRYVCHARNTKGEAEQAQKQKVPAPRYTVEL 360
QY 361 ACGFATVLLVVLIVVYVHYVWLEMLVYFRAHFGTDETLIDGKEYDIYVSVARNABEEEF 420
DB 361 ACGFATVLLVVLIVVYVHYVWLEMLVYFRAHFGTDETLIDGKEYDIYVSVARNABEEEF 420
QY 421 VLLTLRGVLENEFGYKLCIFDRDLSLPGCNTVEAFDFIQRSRMIVLSPDYVTEKSIISM 480
DB 421 VLLTLRGVLENEFGYKLCIFDRDLSLPGGIVTDETLISFIQKSRRLVLSNPNYLQGTQAL 480
QY 481 LEFKLGVMCNSIATK---LIVVEYRPLEHPHGIQLQKES---VSFVSWKGEKSHSG 533
DB 481 LEFKLGVMCNSIATK---LIVVEYRPLEHPHGIQLQKES---VSFVSWKGEKSHSG 533

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Db 481 LELKAGL---ENMASRGNINVLQYKAVKDMK--VKELKRAKTVLTVIKWKGEKSKYPQ 535
Qy 534 SKFWALRLALPLRLSLSSAGWNES 558
Db 536 GRFWKQLQVAMPVKK---SPRWSSN 557

RESULT 9
US-10-282-162-52
; Sequence 52, Application US/10282162
; Publication No. US20030143697A1
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282.162
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 52
; LENGTH: 915
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-282-162-52

Query Match 52.8%; Score 1937.5; DB 4; Length 915;
Best Local Similarity 80.9%; Pred. No. 7.3e-160;
Matches 381; Conservative 11; Mismatches 34; Indels 45; Gaps 7;

Qy 1 MTLWCVVSLYFYGILOSASERCDDWGLDTMRQIQVFEDEPARIKPLFEHFLKFNYS 60
Db 1 MVLWCVVSLYFYGILOSASERCDDWGLDTMRQIQVFEDEPARIKPLFEHFLKFNYS 60
Qy 61 AHSAGLTLIYWTRQDRDLDEEPINFRLPENRISKEKDVLMFRPTLLNDTGNITCMLRNTT 120
Db 61 AHSAGLTLIYWTRQDRDLDEEPINFRLPENRISKEKDVLMFRPTLLNDTGNITCMLRNTT 120
Qy 121 YCSKVAEPLEVVQKSCFNSPMKLPVHKLYIEYGIQRIITCPNVGDPSSVKPTITWYMG 180
Db 121 YCSKVAEPLEVVQKSCFNSPMKLPVHKLYIEYGIQRIITCPNVGDPSSVKPTITWYMG 180
Qy 181 CYKIQNFNNVIPGNNLSFLIALISNNGNYTCVVTYPENGRTFHLTRTLTKVVGSPKNA 240
Db 181 CYKIQNFNNVIPGNNLSFLIALISNNGNYTCVVTYPENGRTFHLTRTLTKVVGSPKNA 240
Qy 241 VPPVIHSPNDHVYKEPGESELLIPCTVYPSFLMDSRNEVWMTIDGKKPDDITIDVTINE 300
Db 241 VPPVIHSPNDHVYKEPGESELLIPCTVYPSFLMDSRNEVWMTIDGKKPDDITIDVTINE 300
Qy 301 SISHSRTEDETRQILSIKVTSEDLKRSVYCHARSAGKGEVAKAAVKQKVPAPRYTVHT 360
Db 301 SISHSRTEDETRQILSIKVTSEDLKRSVYCHARSAGKGEVAKAAVKQKVPAPRYTVHT 360
Qy 361 ----ACGF-----GATVLLVILIVVHVWLEMLVIFYRAHF----- 393
Db 361 GAARSCFRGRHRYKREFRLEGEPAVALRCPQV----PYWLWASVSPRINTLTHKNDKSARTV 416
Qy 394 -GTDETL----DG-----KEYDIYVSYARNABEEFVLLTLRGVLEN 431
Db 417 PGSEETRMMAQDGMALLPALQEDSGTYVCTTRNASYCDKMSIELR-VFEN 466

RESULT 10
US-10-840-138-22
; Sequence 22, Application US/10840138
; Publication No. US20040224893A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Li-Hsien
```

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; APPLICANT: Lin, Hsin Chieh
; APPLICANT: Karow, Margaret
; TITLE OF INVENTION: Methods of Using IL-1 Antagonists to Treat Neointimal Hyperplasia
; FILE REFERENCE: REG 207A
; CURRENT APPLICATION NUMBER: US/10/840.138
; CURRENT FILING DATE: 2004-05-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 915
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-840-138-22
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Query Match 52.8%; Score 1937.5; DB 5; Length 915;
Best Local Similarity 80.9%; Pred. No. 7.3e-160;
Matches 381; Conservative 11; Mismatches 34; Indels 45; Gaps 7;

Qy 1 MTLWCVVSLYFYGILOSASERCDDWGLDTMRQIQVFEDEPARIKPLFEHFLKFNYS 60
Db 1 MVLWCVVSLYFYGILOSASERCDDWGLDTMRQIQVFEDEPARIKPLFEHFLKFNYS 60
Qy 61 AHSAGLTLIYWTRQDRDLDEEPINFRLPENRISKEKDVLMFRPTLLNDTGNITCMLRNTT 120
Db 61 AHSAGLTLIYWTRQDRDLDEEPINFRLPENRISKEKDVLMFRPTLLNDTGNITCMLRNTT 120
Qy 121 YCSKVAEPLEVVQKSCFNSPMKLPVHKLYIEYGIQRIITCPNVGDPSSVKPTITWYMG 180
Db 121 YCSKVAEPLEVVQKSCFNSPMKLPVHKLYIEYGIQRIITCPNVGDPSSVKPTITWYMG 180
Qy 181 CYKIQNFNNVIPGNNLSFLIALISNNGNYTCVVTYPENGRTFHLTRTLTKVVGSPKNA 240
Db 181 CYKIQNFNNVIPGNNLSFLIALISNNGNYTCVVTYPENGRTFHLTRTLTKVVGSPKNA 240
Qy 241 VPPVIHSPNDHVYKEPGESELLIPCTVYPSFLMDSRNEVWMTIDGKKPDDITIDVTINE 300
Db 241 VPPVIHSPNDHVYKEPGESELLIPCTVYPSFLMDSRNEVWMTIDGKKPDDITIDVTINE 300
Qy 301 SISHSRTEDETRQILSIKVTSEDLKRSVYCHARSAGKGEVAKAAVKQKVPAPRYTVHT 360
Db 301 SISHSRTEDETRQILSIKVTSEDLKRSVYCHARSAGKGEVAKAAVKQKVPAPRYTVHT 360
Qy 361 ----ACGF-----GATVLLVILIVVHVWLEMLVIFYRAHF----- 393
Db 361 GAARSCFRGRHRYKREFRLEGEPAVALRCPQV----PYWLWASVSPRINTLTHKNDKSARTV 416
Qy 394 -GTDETL----DG-----KEYDIYVSYARNABEEFVLLTLRGVLEN 431
Db 417 PGSEETRMMAQDGMALLPALQEDSGTYVCTTRNASYCDKMSIELR-VFEN 466
```

```
RESULT 11
US-10-945-068-22
; Sequence 22, Application US/10945068
; Publication No. US20050129685A1
; GENERAL INFORMATION:
; APPLICANT: Jingtai Cao
; APPLICANT: Stanley J. Wiegand
; TITLE OF INVENTION: USE OF IL-1 BLOCKERS TO PREVENT CORNEAL INFLAMMATION
; FILE REFERENCE: REG 208A
; CURRENT APPLICATION NUMBER: US/10/945.068
; CURRENT FILING DATE: 2004-09-20
; PRIOR APPLICATION NUMBER: 60/503.854
; PRIOR FILING DATE: 2003-09-18
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 915
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-945-068-22
```


Query Match	52.8%;	Score 1937.5;	DB 5;	Length 915;
Best Local Similarity	80.9%;	Pred. No. 7.3e-160;		
Matches 381;	Conservative 11;	Mismatches 34;	Indels 45;	Gaps 7

Qy	1	MTLLWCVVSLFYGYGLQSDASERCDDGLDTRMQIQVFEDEPARIKCPLFEHFLKFNYST	60
Db	1	MVLWCVVSLFYGYGLQSDASERCDDGLDTRMQIQVFEDEPARIKCPLFEHFLKFNYST	60
Qy	61	AHSAGLTLIWIWTRQDRDLEEPINFRLENRISKEKDVLFWFRPTLLNDTGNVTCMLRNTT	120
Db	61	AHSAGLTLIWIWTRQDRDLEEPINFRLENRISKEKDVLFWFRPTLLNDTGNVTCMLRNTT	120
Qy	121	YCSKVAPFLEVQKDCSFCNSPMKLPVHKLYIEYGIQIRITCPNVGDFPSSVKPTITWYMG	180
Db	121	YCSKVAPFLEVQKDCSFCNSPMKLPVHKLYIEYGIQIRITCPNVGDFPSSVKPTITWYMG	180
Qy	181	CYKIQNFNNVPIEGNMNLSFLALISNNGNYTCVVTYPENGRTFHLTRILTVKVGSPKNA	240
Db	181	CYKIQNFNNVPIEGNMNLSFLALISNNGNYTCVVTYPENGRTFHLTRILTVKVGSPKNA	240
Qy	241	VPPVIHSDNHVYKEPGEELLIPCTVYFSLMDSRNEVWMTIDGKKPDDITIDVTINE	300
Db	241	VPPVIHSDNHVYKEPGEELLIPCTVYFSLMDSRNEVWMTIDGKKPDDITIDVTINE	300
Qy	301	SISHSRTEDETRTQILSKVTSIEDLKRSYVCHARSAKGEVAKAAVKQKVPAPRYTVEL	360
Db	301	SISHSRTEDETRTQILSKVTSIEDLKRSYVCHARSAKGEVAKAAVKQKVPAPRYTVHT	360
Qy	361	-----ACGF-----GATVLLVVLIVVYHVYVLEWVLFYRAHF-----	393
Db	361	GAASRCFRGRHYKREPRLECEPVALRCPQV----PYWLMAVSVPRI NLTHWKNDARSATV	416
Qy	394	-GTDETIL----DG-----KEYDIVSVYARNABEEFVLLTLRGVLEN	431
Db	417	PGEESTRMADGALWLLPALQEDSGTVCVCTRNASYCDKMSIELR-VFEN	466

```

RESULT 12
US-11-056-730-22
; Sequence 22, Application US/11056730
; Publication No. US20050197293A1
; GENERAL INFORMATION:
; APPLICANT: Mellis, Scott
; APPLICANT: Stahl, Neil
; APPLICANT: Radin, Allen
; APPLICANT: Weinstein, Steven
; APPLICANT: Calaprice, Denise
; APPLICANT: Karow, Margaret
; APPLICANT: Papadopoulos, Joanne
; TITLE OF INVENTION: Use of an IL-1 Antagonist for Treating Arthritis
; FILE REFERENCE: 203G
; CURRENT APPLICATION NUMBER: US/11/056,730
; CURRENT FILING DATE: 2005-02-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 915
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-11-056-730-22

```

```

Db      61 AHSAGLTLIYWYTRQDRDLBEPINFLPENRISKEKDLWFRPTLLDNGNYTCMLRNTT 120
QY      121 YCSKVAFLEVVQKDCSFNSPMKLPVKLYIEYQIRITCPNVDGYFPSSVKPTITWYMG 180
Db      121 YCSKVAFLEVVQKDCSFNSPMKLPVKLYIEYQIRITCPNVDGYFPSSVKPTITWYMG 180
QY      181 CYKIONFNNVIPEGNMLSFLIALISNNGNYTCVVTYPENGRTFHLTRTLTVKVGSPKNA 240
Db      181 CYKIONFNNVIPEGNMLSFLIALISNNGNYTCVVTYPENGRTFHLTRTLTVKVGSPKNA 240
QY      241 VPPVIHSDNDHVHYEKEPEGELLIPCTVYFSEFLMSDRNEVWMTIDGKKPDDITIDVTINE 300
Db      241 VPPVIHSDNDHVHYEKEPEGELLIPCTVYFSEFLMSDRNEVWMTIDGKKPDDITIDVTINE 300
QY      301 SISHSRTEDETRTQILSIKKVTSIDLKRSYVCHARSAGEVAKAAKVQKVPAPRYTVEL 360
Db      301 SISHSRTEDETRTQILSIKKVTSIDLKRSYVCHARSAGEVAKAAKVQKVPAPRYTVHT 360
QY      361 ----ACGF-----GATVLLLVILIVVHYVWLEWLVFRAHF----- 393
Db      361 GAARSCRFGRHYKREPRLEGEPAVLRCPQV----PYWLWASVSPRINLTWHKNDARSATV 416
QY      394 -GTDETIL---DG-----KEYDIIVSVYARNAEFEFVLLTLRGVLEN 431
Db      417 PGEETRMAODGALWLLPALQDSGTVCTTRNASYCDKMSIELR-VFEN 466

RESULT 13
US-11-134-114-52
; Sequence 52, Application US/11134114
; Publication No. US2005022033A1
; GENERAL INFORMATION:
; APPLICANT: Stahl, Neil
; APPLICANT: Yancopoulos, George D.
; TITLE OF INVENTION: Receptor Based Antagonists and Methods of Making and Using
; FILE REFERENCE: 203C1
; CURRENT APPLICATION NUMBER: US/11/134,114
; CURRENT FILING DATE: 2005-05-20
; PRIOR APPLICATION NUMBER: 10/282,162
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 52
; LENGTH: 915
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-134-114-52

```

```
Db 181 CYKIQNFNNVPEGMNLSFLIALISNNGNYTCVVYTPENGRTFHLTRTLTVKVVGSPKNA 240
Qy 241 VPPVIHSPNDHVYKEPGEELLIPCTVYFSLMDSRNEVWMTIDGKKPDDITIDVTINE 300
Db 241 VPPVIHSPNDHVYKEPGEELLIPCTVYFSLMDSRNEVWMTIDGKKPDDITIDVTINE 300
Qy 301 SISHSRTEDETRTQILSIKKVTSDDLKRSYVCHARSAGKGEVAKAAVKQKVPAPRYTVEL 360
Db 301 SISHSRTEDETRTQILSIKKVTSDDLKRSYVCHARSAGKGEVAKAAVKQKVPAPRYTVHT 360
Qy 361 ----ACGF-----GATVLLVVLIVVHVWVLEWLVFYRAHF----- 393
Db 361 GAARSCRFRGRHRYKREFRLEGEPAVALRCPQV-----PYWLWASVSPRINLTWHKNDARSATV 416
Qy 394 -GTDETL-----DG-----KEYDIYVSVARNABEEEEFFVLLTLRGVLEN 431
Db 417 PGEETRMAQDAGALLPALQEDSGTYVCTTRNASYCDKMSIELR-VFEN 466

RESULT 14
US-10-282-162-54
; Sequence 54, Application US/10282162
; Publication No. US20030143697A1
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282,162
; PRIOR FILING DATE: 2002-10-28
; PRIOR FILING DATE: 1999-09-22
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 54
; LENGTH: 917
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-282-162-54

Query Match 52.8%; Score 1937.5; DB 4; Length 917;
Best Local Similarity 80.9%; Pred. No. 7.3e-150;
Matches 381; Conservative 11; Mismatches 34; Indels 45; Gaps 7;

Qy 1 MTLWCVSVLYFYGILOSDASERCDDGLDMRQIQVFEDEPARIKCPLFEHFLKFNYS 60
Db 1 MVLWCVSVLYFYGILOSDASERCDDGLDMRQIQVFEDEPARIKCPLFEHFLKFNYS 60
Qy 61 AHSAGLTLIYWTRQDRDLLEPINFRLPENRISKEKDVLMFRPTLLNDTGNITCMLRNTT 120
Db 61 AHSAGLTLIYWTRQDRDLLEPINFRLPENRISKEKDVLMFRPTLLNDTGNITCMLRNTT 120
Qy 121 YCSKVAPPLEVWQKSCFNSPMKLPVHKLYIEYGIQRIITCPNVGDGYPPSSVKPTITWYMG 180
Db 121 YCSKVAPPLEVWQKSCFNSPMKLPVHKLYIEYGIQRIITCPNVGDGYPPSSVKPTITWYMG 180
Qy 181 CYKIQNFNNVPEGMNLSFLIALISNNGNYTCVVYTPENGRTFHLTRTLTVKVVGSPKNA 240
Db 181 CYKIQNFNNVPEGMNLSFLIALISNNGNYTCVVYTPENGRTFHLTRTLTVKVVGSPKNA 240
Qy 241 VPPVIHSPNDHVYKEPGEELLIPCTVYFSLMDSRNEVWMTIDGKKPDDITIDVTINE 300
Db 241 VPPVIHSPNDHVYKEPGEELLIPCTVYFSLMDSRNEVWMTIDGKKPDDITIDVTINE 300
Qy 301 SISHSRTEDETRTQILSIKKVTSDDLKRSYVCHARSAGKGEVAKAAVKQKVPAPRYTVEL 360
Db 301 SISHSRTEDETRTQILSIKKVTSDDLKRSYVCHARSAGKGEVAKAAVKQKVPAPRYTVHT 360
Qy 361 ----ACGF-----GATVLLVVLIVVHVWVLEWLVFYRAHF----- 393
Db 361 GAARSCRFRGRHRYKREFRLEGEPAVALRCPQV-----PYWLWASVSPRINLTWHKNDARSATV 416
Qy 394 -GTDETL-----DG-----KEYDIYVSVARNABEEEEFFVLLTLRGVLEN 431
Db 417 PGEETRMAQDAGALLPALQEDSGTYVCTTRNASYCDKMSIELR-VFEN 466

Search completed: December 7, 2005, 13:47:02
Job time : 170 secs
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```
Db 361 GAARSCRFRGRHRYKREFRLEGEPAVALRCPQV-----PYWLWASVSPRINLTWHKNDARSATV 416
Qy 394 -GTDETL-----DG-----KEYDIYVSVARNABEEEEFFVLLTLRGVLEN 431
Db 417 PGEETRMAQDAGALLPALQEDSGTYVCTTRNASYCDKMSIELR-VFEN 466

RESULT 15
US-10-282-162-56
; Sequence 56, Application US/10282162
; Publication No. US20030143697A1
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282,162
; PRIOR FILING DATE: 2002-10-28
; PRIOR FILING DATE: 1999-09-22
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 56
; LENGTH: 917
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-282-162-56

Query Match 52.8%; Score 1937.5; DB 4; Length 917;
Best Local Similarity 80.9%; Pred. No. 7.3e-160;
Matches 381; Conservative 11; Mismatches 34; Indels 45; Gaps 7;

Qy 1 MTLWCVSVLYFYGILOSDASERCDDGLDMRQIQVFEDEPARIKCPLFEHFLKFNYS 60
Db 1 MVLWCVSVLYFYGILOSDASERCDDGLDMRQIQVFEDEPARIKCPLFEHFLKFNYS 60
Qy 61 AHSAGLTLIYWTRQDRDLLEPINFRLPENRISKEKDVLMFRPTLLNDTGNITCMLRNTT 120
Db 61 AHSAGLTLIYWTRQDRDLLEPINFRLPENRISKEKDVLMFRPTLLNDTGNITCMLRNTT 120
Qy 121 YCSKVAPPLEVWQKSCFNSPMKLPVHKLYIEYGIQRIITCPNVGDGYPPSSVKPTITWYMG 180
Db 121 YCSKVAPPLEVWQKSCFNSPMKLPVHKLYIEYGIQRIITCPNVGDGYPPSSVKPTITWYMG 180
Qy 181 CYKIQNFNNVPEGMNLSFLIALISNNGNYTCVVYTPENGRTFHLTRTLTVKVVGSPKNA 240
Db 181 CYKIQNFNNVPEGMNLSFLIALISNNGNYTCVVYTPENGRTFHLTRTLTVKVVGSPKNA 240
Qy 241 VPPVIHSPNDHVYKEPGEELLIPCTVYFSLMDSRNEVWMTIDGKKPDDITIDVTINE 300
Db 241 VPPVIHSPNDHVYKEPGEELLIPCTVYFSLMDSRNEVWMTIDGKKPDDITIDVTINE 300
Qy 301 SISHSRTEDETRTQILSIKKVTSDDLKRSYVCHARSAGKGEVAKAAVKQKVPAPRYTVEL 360
Db 301 SISHSRTEDETRTQILSIKKVTSDDLKRSYVCHARSAGKGEVAKAAVKQKVPAPRYTVHT 360
Qy 361 ----ACGF-----GATVLLVVLIVVHVWVLEWLVFYRAHF----- 393
Db 361 GAARSCRFRGRHRYKREFRLEGEPAVALRCPQV-----PYWLWASVSPRINLTWHKNDARSATV 416
Qy 394 -GTDETL-----DG-----KEYDIYVSVARNABEEEEFFVLLTLRGVLEN 431
Db 417 PGEETRMAQDAGALLPALQEDSGTYVCTTRNASYCDKMSIELR-VFEN 466

Search completed: December 7, 2005, 13:47:02
Job time : 170 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 7, 2005, 13:34:02 ; Search time 12 Seconds
(without alignments)
319.708 Million cell updates/sec

Title: US-10-061-727-2
Perfect score: 3669
Sequence: 1 MTLWCVVSLFYGILQSDA.....SALAHHTDLSNNDFVIL 687

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 32527 seqs, 5584426 residues

Total number of hits satisfying chosen parameters: 32527

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA New:

- 1: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	252	6.9	398	6	US-10-821-234-1583
2	148	4.0	7968	7	US-11-186-731-5
3	130	3.5	1049	6	US-10-131-826A-358
4	121	3.3	879	7	US-11-022-562-340
5	121	3.3	1338	6	US-10-821-234-1622
6	115	3.1	1338	7	US-11-109-156-23
7	111	3.0	1119	6	US-10-131-826A-352
8	109	3.0	583	7	US-11-080-991-64
9	108	2.9	532	7	US-11-104-812-2
10	106	2.9	532	7	US-11-103-279-2
11	106	2.9	567	7	US-11-016-503-10
12	106	2.9	2828	7	US-11-080-991-54
13	106	2.9	2828	7	US-11-186-284-49
14	105	2.9	1694	7	US-11-135-855-36
15	105	2.9	1709	7	US-11-135-855-35
16	103	2.8	567	7	US-11-016-503-2
17	101	2.8	1032	7	US-11-014-367-2
18	100	2.7	4419	6	US-10-821-234-1155
19	98.5	2.7	455	7	US-11-016-503-14
20	98.5	2.7	455	7	US-11-089-803-4
21	97.5	2.7	409	6	US-10-821-234-892
22	97	2.6	557	7	US-11-016-503-4
23	97	2.6	985	7	US-11-113-424-61
24	96.5	2.6	1250	7	US-11-137-465-62
25	95	2.6	462	7	US-11-016-503-8

26	94.5	2.6	740	7	US-11-137-465-61	Sequence 61, Appl
27	94	2.6	1897	6	US-10-821-234-1635	Sequence 1635, Ap
28	94	2.6	1907	7	US-11-000-463-250	Sequence 250, App
29	92.5	2.5	300	7	US-11-025-834A-21	Sequence 21, Appl
30	92.5	2.5	649	7	US-11-102-240-132	Sequence 132, App
31	92.5	2.5	1032	7	US-11-014-367-3	Sequence 3, Appl
32	91.5	2.5	326	6	US-10-999-866-36	Sequence 36, Appl
33	91.5	2.5	326	7	US-11-144-248-28	Sequence 28, Appl
34	91.5	2.5	326	7	US-11-061-821-36	Sequence 36, Appl
35	91.5	2.5	470	7	US-11-144-248-45	Sequence 45, Appl
36	91.5	2.5	470	7	US-11-144-248-46	Sequence 46, Appl
37	91.5	2.5	470	7	US-11-144-248-49	Sequence 49, Appl
38	91.5	2.5	473	7	US-11-144-248-50	Sequence 50, Appl
39	91.5	2.5	983	7	US-11-113-424-59	Sequence 59, Appl
40	91	2.5	450	6	US-10-131-826A-378	Sequence 378, App
41	90.5	2.5	450	7	US-11-025-712-12	Sequence 12, Appl
42	90.5	2.5	477	6	US-10-131-826A-50	Sequence 50, Appl
43	90.5	2.5	628	7	US-11-080-991-108	Sequence 108, App
44	90.5	2.5	1032	6	US-10-835-475-1	Sequence 1, Appl
45	90.5	2.5	1032	7	US-11-014-367-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-10-821-234-1583
; Sequence 1583, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821.234
; PRIOR FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1583
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-821-234-1583

Query Match	6.9%	Score 252;	DB 6;	Length 398;
Best Local Similarity	23.4%	Pred. No. 4e+15;		
Matches	79;	Conservative	51;	Mismatches 148; Indels 60; Gaps 13;
Qy	20	ASERCDWGLDTRQIQVFEDEPARIKCPLEHFKFNYSHTAHAGLTLIWTQRDRL	79	
Db	24	AARSCRPRGRHYKREFRL-EGEPVALRCPPVYWLWASVSPR----INLTWHKNDARSIV	78	
Qy	80	--EPIPNFRLEPNRISKEKDVLPWERTLLNDTGNVTCMLNNTTYCSKVAFPLEVYQKDCS	137	
Db	79	PGEE-----ETRMWAQDQALMLLPALQEDSGYVCTTRNASYCDKMSIELRVFNTDA	131	
Qy	138	FNSPMKPLVPHKLYIEY-----GIQRITCPNVGDYFPSSVKPTITWYMGCYKIQNFN	188	
Db	132	F-----LP-----FISYPQILTSLTSGV--LVCPDLSEFRDKTDVKIQWKDLSLLDKDN	180	
Qy	189	NVPEGNLNFSLI---ALISNNGNYTCVTPYENGRTFHLTRTLTVKVVGSPKNAVPVI	245	
Db	181	EKFLSVRGTTLLVHDVALEDAGYRCVLTFAHEGQQYNITRSIELRIKKKEETI-EVI	239	
Qy	246	HSPNDHVVYEKPEGEELLIPCTVYFSLMDSRNVMWTIDGKKPDDITDVTINESISHS	305	
Db	240	ISPUKTI--SASLSRLTIPCKVFLGTPLTTLMMWTAN-----DTHISSAYPGG	288	
Qy	306	RTEDETRTQI-----LSIKKVTSEDLKRSYVC	332	

Qy 433 FGYKLCIFDRDLSLPGGNTVEAVDFIQBS-----RRMIVVLSDDYVTEKSIIMLEFKLGM- 488
 Db 833 LG-----RGAF--GKVVQASAFGIKKSPCTRTVAVKMLKEGATASEYKALMTLKILT 883
 Qy 489 -----CONSIATKLIWEX-----RPLEHPHGILQKESVSFVSKGE 527
 Db 884 HIGHHLNVNLLGACTKGGPLMVIVEYCKYGNLSYKSKRDLFFLNKDAALHMEPKKE 943
 Qy 528 KSKHSGKFKWALRLALPLRLSLS--ASSGWNESCSQSDISLDHVQRRSR--LKEP 580
 Db 944 KWE-PGLEQGGKPRLDSTVTSSEFASGFG-----QEDKSLSDVEEEDSDGFYKEP 993

RESULT 6
 US-11-109-156-23
 ; Sequence 23, Application US/11109156
 ; Publication No. US20050250144A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Toshio Ota
 ; APPLICANT: Takao Isogai
 ; APPLICANT: Tetsuo Nishikawa
 ; APPLICANT: Koji Hayashi
 ; APPLICANT: Kaoru Otsuka
 ; APPLICANT: Jun-Ichi Yamamoto
 ; APPLICANT: Shizuko Ishii
 ; APPLICANT: Tomoyasu Sugiyama
 ; APPLICANT: Ai Wakamatsu
 ; APPLICANT: Keiichi Nagai
 ; APPLICANT: Tetsuji Otsuki
 ; APPLICANT: Shin-Ichi Funahashi
 ; APPLICANT: Chiaki Senoo
 ; APPLICANT: Jun-ichi Nezu
 ; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTEIN
 ; TITLE OF INVENTION: PHOSPHATASE
 ; FILE REFERENCE: 06501-099002
 ; CURRENT APPLICATION NUMBER: US/11/109,156
 ; CURRENT FILING DATE: 2005-04-19
 ; PRIOR APPLICATION NUMBER: US/10/060,065
 ; PRIOR FILING DATE: 2002-01-29
 ; PRIOR APPLICATION NUMBER: PCT/JP00/05061
 ; PRIOR FILING DATE: 2000-07-28
 ; PRIOR APPLICATION NUMBER: US 60/159,590
 ; PRIOR FILING DATE: 1999-10-18
 ; PRIOR APPLICATION NUMBER: US 60/183,322
 ; PRIOR FILING DATE: 2000-02-17
 ; PRIOR APPLICATION NUMBER: JP 11-248036
 ; PRIOR FILING DATE: 1999-07-29
 ; PRIOR APPLICATION NUMBER: JP 2000-118776
 ; PRIOR FILING DATE: 2000-01-11
 ; PRIOR APPLICATION NUMBER: JP 2000-183767
 ; PRIOR FILING DATE: 2000-05-02
 ; PRIOR APPLICATION NUMBER: JP 2000-241899
 ; PRIOR FILING DATE: 2000-06-09
 ; NUMBER OF SEQ ID NOS: 43
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 23
 ; LENGTH: 1338
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-109-156-23

Query Match 3.1%; Score 115; DB 7; Length 1338;
 Best Local Similarity 20.5%; Pred. No. 0.038;
 Matches 136; Conservative 68; Mismatches 199; Indels 262; Gaps 34;

Qy 108 DTGNTCML-----RNTTYSKVAFFLEVQKD--SCFNSPMKLPVHKLYI-----EYG 154
 Db 399 DAGNYTILLSIKNSVFNKLTALIVNKPQIYEKAVSSPPDPAIPLGSRQILCTAYG 458
 Qy 155 IQRITCNVDGYPSSVVKPTITWY-----MGCKYI 184
 Db 459 IP-----OPTIKFWHPCHNHSEARCDFCNSNEESFILDADSNMG-NRI 502

Qy 185 QNFNN--VIEGWN--LSFLIALISN--NGNYTCVVVYPENGRTFHLTRTLTVKVGSPKN 239
 Db 503 ESITORMAITEGKNKMASTLVADSRISGIYICASN-----KVGTVG--RN 547
 Qy 240 AVPPVIHSPND--HVVYEKEP--GBELLIPTVVFSLMDSRNEVWV-----TIDCK----- 287
 Db 548 ISFYITDVPNGFHNLEKMPTEGEDDLKLSCTVN--KFLY-----RDVTWILLRTVNNRTWHYS 603
 Qy 288 -----KPDITIDVTI--NESISHSRT-----EDTTRTQILSIKKVTSETDLKRSYV 331
 Db 604 ISKQKMAITKEHSITLNLTIMNVSLQDSGYACRARNVYTGEELLOKKEITIRDOEAPYL 663
 Qy 332 -----CHARSAGEVAKAAVKQKVPAPRYT-----VELAC 362
 Db 664 LRNLSDHITVAISSSTTLDCHANG-----VPEQITWFKNNHKIQQEPGIL 709
 Qy 363 GFGATVLLVILIV---VYHVYVWLEMLVYRAHFGTDEITLDGKEYDIYVSYARNABEE 418
 Db 710 GPGSSTLFIERVTEDEGVYHCK-----ATNQK--GSVSSAYLTVOGTSDKS 755
 Qy 419 EFVLLTL-----RGVLENEFGYKLCIFDRDLSL----- 446
 Db 756 NLELITLTCTCVAATLFWLLLTLLIRKMKSSSEIKTDYLSIIMDPDEVLDEQCERLPY 815
 Qy 447 -----GGNTVEAVDFDIORS-----RRMIVVLSDDYVTEKSIISML 481
 Db 816 DASKWBFARERLKLKSLGRGAFGKVVQASAFGIKKSPCTRTVAVKMLKEGATASEYKAL 875
 Qy 482 EFKLGM-----CONSIATKLIWEX-----RPLEHPHGILQKESV 519
 Db 876 MTEKLITLTHIGHHLNVNLLGACTKGGPLMVIVEYCKYGNLSYKSKRDLFFLNKDA 935
 Qy 520 SFVSWGKSKHSGKFKWALRLALPLRLSLS--ASSGWNESCSQSDISLDHVQRRSR-- 576
 Db 936 LHMEPKKEKWE-PGLEQGGKPRLDSTVTSSEFASGFG-----QEDKSLSDVEEEDSDG 988
 Qy 577 -LKEP 580
 Db 989 FYKEP 993

RESULT 7
 US-10-131-826A-352
 ; Sequence 352, Application US/10131826A
 ; Publication No. US20050245730A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Beresini, Maureen
 ; APPLICANT: DeForge, Laura
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Sherwood, Steven
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K
 ; APPLICANT: Wood, William
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: ACIDS ENCODING THE SAME
 ; FILE REFERENCE: P330R1C128
 ; CURRENT APPLICATION NUMBER: US/10/131,826A
 ; CURRENT FILING DATE: 2002-04-24
 ; PRIOR APPLICATION NUMBER: 60/049911
 ; PRIOR FILING DATE: 1997-06-18
 ; PRIOR APPLICATION NUMBER: 60/056974
 ; PRIOR FILING DATE: 1997-08-26

[illegible]

```
; Sequence 2, Application US/11104812
; Publication No. US20050260153A1
; GENERAL INFORMATION:
; APPLICANT: CALIAS, PERICLES
; APPLICANT: COOK, GARY P.
; APPLICANT: SHIMA, DAVID T.
; APPLICANT: TURNER, DAVID I.
; APPLICANT: GANLEY, MARY A.
; TITLE OF INVENTION: FACILITATION OF IONTOPHORESIS USING CHARGED MOIETIES
; FILE REFERENCE: EYE-035D1V
; CURRENT APPLICATION NUMBER: US/11/104,812
; CURRENT FILING DATE: 2005-04-13
; PRIOR APPLICATION NUMBER: 60/561,601
; PRIOR FILING DATE: 2004-04-13
; PRIOR APPLICATION NUMBER: 60/658,819
; PRIOR FILING DATE: 2005-03-04
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 2
; LENGTH: 532
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-104-812-2

Query Match      2.9%; Score 108; DB 7; Length 532;
Best Local Similarity 22.3%; Pred. No. 0.042;
Matches 73; Conservative 38; Mismatches 94; Indels 122; Gaps 17;

Qy 106 LNDTGNVTCMLRNTTYGSKVAFPLEVVQKDCSCFNSPMKLPVHKLYIBYGIQRTICPNVDG 165
Db 259 LNPTVTY----GNDSPSAKAS--VSVTAED-----GTQRLTCAVILG 295
Qy 166 YFPSSVKPTITWYMGCKYKQNF--NNVI-----PEGNLSFLI-----ALISNNG--- 208
Db 296 NQSOETLQTVTIY-----SFPAPNVILTKPEVSEGTETVTKCEAHPRAKVTILNGVPAQ 348
Qy 209 -----NYTCVVTYPENGRTFHLTRTLTKVVGSPKNAVPPVHSPNDHVYVEKEPEEEL 262
Db 349 PLGPRAQLLKATPEDNGRSFSCSATL--EVAGQ-----LIH-----KNQTRREL 390
Qy 263 LIPCTVYFSLMDSR-----NEVWMTIDGKKP-----DDITIDVTINESIS 303
Db 391 ----RVLYGPRLDERDCPGNWTWPENSQQTPMCQAWGNPLPELCKLDGTFPLPAGESVT 446
Qy 304 HSRTEDTRTQILSIKKVTSSEDLKRSYVCHARSAGKGEVAKAAVKQKVPAPRYTVLACG 363
Db 447 VTR-----DLEGTYLCRARSTQGEVTR--EVTNVLSPRVEI----- 481
Qy 364 FGATVLLVILIVVYHYVWLEWMLFYR 390
Db 482 ---VIITVVAAVIMGTAGLSTLYNLR 505

RESULT 10
US-11-105-279-2
; Sequence 2, Application US/11105279
; Publication No. US20050260651A1
; GENERAL INFORMATION:
; APPLICANT: CALIAS, PERICLES
; APPLICANT: COOK, GARY P.
; APPLICANT: SHIMA, DAVID T.
; APPLICANT: ADAMIS, ANTHONY P.
; APPLICANT: NG, YIN-SHAN
; APPLICANT: ROBINSON, GREGORY S.
; APPLICANT: TURNER, DAVID I.
; APPLICANT: GANLEY, MARY A.
; TITLE OF INVENTION: ENHANCED BIOLOGICALLY ACTIVE CONJUGATES
; FILE REFERENCE: EYE-035
; CURRENT APPLICATION NUMBER: US/11/105,279
; CURRENT FILING DATE: 2005-04-13
; PRIOR APPLICATION NUMBER: 60/561,601
; PRIOR FILING DATE: 2004-04-13
; PRIOR APPLICATION NUMBER: 60/658,819

; Sequence 2, Application US/11104812
; Publication No. US20050260153A1
; GENERAL INFORMATION:
; APPLICANT: CALIAS, PERICLES
; APPLICANT: COOK, GARY P.
; APPLICANT: SHIMA, DAVID T.
; APPLICANT: TURNER, DAVID I.
; APPLICANT: GANLEY, MARY A.
; TITLE OF INVENTION: FACILITATION OF IONTOPHORESIS USING CHARGED MOIETIES
; FILE REFERENCE: EYE-035D1V
; CURRENT APPLICATION NUMBER: US/11/104,812
; CURRENT FILING DATE: 2005-04-13
; PRIOR APPLICATION NUMBER: 60/561,601
; PRIOR FILING DATE: 2004-04-13
; PRIOR APPLICATION NUMBER: 60/658,819
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 2
; LENGTH: 532
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-105-279-2

Query Match      2.9%; Score 108; DB 7; Length 532;
Best Local Similarity 22.3%; Pred. No. 0.042;
Matches 73; Conservative 38; Mismatches 94; Indels 122; Gaps 17;

Qy 106 LNDTGNVTCMLRNTTYGSKVAFPLEVVQKDCSCFNSPMKLPVHKLYIBYGIQRTICPNVDG 165
Db 259 LNPTVTY----GNDSPSAKAS--VSVTAED-----GTQRLTCAVILG 295
Qy 166 YFPSSVKPTITWYMGCKYKQNF--NNVI-----PEGNLSFLI-----ALISNNG--- 208
Db 296 NQSOETLQTVTIY-----SFPAPNVILTKPEVSEGTETVTKCEAHPRAKVTILNGVPAQ 348
Qy 209 -----NYTCVVTYPENGRTFHLTRTLTKVVGSPKNAVPPVHSPNDHVYVEKEPEEEL 262
Db 349 PLGPRAQLLKATPEDNGRSFSCSATL--EVAGQ-----LIH-----KNQTRREL 390
Qy 263 LIPCTVYFSLMDSR-----NEVWMTIDGKKP-----DDITIDVTINESIS 303
Db 391 ----RVLYGPRLDERDCPGNWTWPENSQQTPMCQAWGNPLPELCKLDGTFPLPAGESVT 446
Qy 304 HSRTEDTRTQILSIKKVTSSEDLKRSYVCHARSAGKGEVAKAAVKQKVPAPRYTVLACG 363
Db 447 VTR-----DLEGTYLCRARSTQGEVTR--EVTNVLSPRVEI----- 481
Qy 364 FGATVLLVILIVVYHYVWLEWMLFYR 390
Db 482 ---VIITVVAAVIMGTAGLSTLYNLR 505

RESULT 11
US-11-016-503-10
; Sequence 10, Application US/11016503
; Publication No. US2005024547A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Papadopoulos et al.
; TITLE OF INVENTION: MODIFIED CHIMERIC POLYPEPTIDES WITH IMPROVED
; TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES AND METHODS OF MAKING
; TITLE OF INVENTION: AND USING THEREOF
; FILE REFERENCE: REG 710-A-US
; CURRENT APPLICATION NUMBER: US/11/016,503
; CURRENT FILING DATE: 2004-12-17
; PRIOR APPLICATION NUMBER: US/10/009,852
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: PCT/US00/14142
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/138,133
; PRIOR FILING DATE: 1999-06-08
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 567
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-016-503-10

Query Match      2.9%; Score 106; DB 7; Length 567;
Best Local Similarity 19.6%; Pred. No. 0.069;
Matches 86; Conservative 49; Mismatches 132; Indels 172; Gaps 22;

Qy 87 LPENRISKEDVILWFRPTLLNDTGNVTC--MLRNTTY-----CSKVAFPL-----EVV 132
Db 63 LPE-MVSKESERLSITKSACGRNGKQFCSTLTTLTAQANHGTGYSCKYLAVPTSKKETE 121
Qy 133 QKDCSCFNSPMKLPVHKLYIEY-----GIQ-----RITCPNVDGFFSSVPTITWYM 179
```



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Db 122 SAIYIFISDTGRPFVEMYSEIPEIIMTEGRELVPCRVTSNI-----IVT--- 168
QY 180 GCYKIONF--NNVIPGNNL-----SFLI--ALISNNNGYTCVVT-----YPENGRFTH 224
Db 169 -----LKKFPLDLTLPDGKRIIWDNRKGFIIISNATYKEIGLLTCEATVNGHLKYNTYLTHR 224
QY 225 LRTLTIVKVVGPKNVAVPVIHSPNDHVVEKEPGEELLIPCTVYFSLMDSRNEVWWTI 284
Db 225 QINTIIDVOISPR---PV-----KLLRGHTLVNCTA--TTPLNTRVQNTWSY 268
QY 285 DGKKPDIDITVINESISHSRTEDTRQIILSIKKVTSSEDLKRSYVCHARS----- 336
Db 269 -----PDEKNKNASVRRRIIDQSNHANI FYSVLITDKMQNKD-KGLYTCRVRSRSPGSKSVN 323
QY 337 -----AKGEVAKAAKVKQVPAP-----RVTVELAC-- 362
Db 324 TSVHIYDKAGPEKSCDKTHTCPCPAPELLGGPSVFLFPKPKDITLMISRTPEVTCVV 383
QY 363 -----GFGATVLLAVLILVYVHYVWLEWLVFYRA 391
Db 384 VDVSHPDKVKNWYVDGVEVINAKTKPREQNSTYRVSVLTVL-HQDW----- 433
QY 392 HFGTDETLIDGKEYDIYS 410
Db 434 -----LNGKEYCKVS 444
```

```
RESULT 12
US-11-080-991-54
; Sequence 54, Application US/11080991
; Publication No. US20050266437A1
; GENERAL INFORMATION:
; APPLICANT: Veiby, Petter Ole
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR
; FILE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST
; TITLE OF INVENTION: AND OVARIAN CANCER
; CURRENT FILING DATE: 2005-03-11
; PRIOR FILING DATE: 2005-03-11
; PRIOR FILING DATE: 2002-06-21
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 54
; LENGTH: 2828
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-080-991-54
```

```
Query Match 2.9%; Score 106; DB 7; Length 2828;
Best Local Similarity 22.2%; Pred. No. 0.71;
Matches 108; Conservative 56; Mismatches 157; Indels 166; Gaps 30;

QY 72 WTRQDRDLLEEFNPLPENRI-----SKEKDVLMFRPTLL-----NDTGNVTCMLR 117
Db 2175 WPR-----ILWRLPSKRMIDALFSDSRK--VFANGTLVVKSVTKDAGDYLCVAR 2224
QY 118 NTTYCSKVAPLEVVQKDCSCFNSPKMLP-----VHKLYIEYGIORITC-----PNVDGYF 167
Db 2225 NKVGDDYVVLKVDVVMK-----PAKIEHKEENDHKVFG-GDLKVDVCATGLPN----- 2272
QY 168 PSSVVPPTITWYMGCVKION-----FNNVIPEGMNLISFLIALISNNGY 210
Db 2273 -----PEISWSLPGSLVNSFMQSDSGGRTKRYVVFNN-----GTLFYFNEVGMREEGY 2322
QY 211 TCVVITYPEN--GRTHLTRLTVKVGSP---KNAPVPVIHSPNDHVVEKEPGEELLIP 265
Db 2323 TC---FAENQVGKDEMVR---VKVVTAPATIRNKTLYLAVQVPY-----GDVVTVA 2367
QY 266 CTVYFSLMDSRNEVWWTIDGKKPDIDITVINESISHSRTEDTRQIILSIKKVTSSE 325
Db 2368 C-----EAKGEMPKVTWLSP---INKVIPTSSKEYIQVQDGT-----LLIQAQRSD 2412
```

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QY 326 LKRSYVCHARSAKGEVAKAAKVKQV-----PAPRYTV-ELACGFGATVLLVLVIL-- 374
Db 2413 -SGNYTCLVNRSAGEDRKTVMHVNVPQPKINGNPNPITTVREIAAG-GSRKLDICKAEG 2470
QY 375 IVVYHVYWL--EMVLFYRAHFCTDETILDGKEYDIYSYARNAEEREEFVLLTLRGLVLENE 432
Db 2471 IPTPRVLWAFPEGVVLPAHYGNRITVHGNSLDI-----RSLRKSQSVQLVC--MARNE 2523
QY 433 FGKLCIFDRSLPGNGTVEAVDFIQSRRMIV---VLSP-----DYVTEKISIMLE 482
Db 2524 GG-----EARLIVQLTVLEPMEKPIFHPDISEKITAMAG 2557
QY 483 FKLGVMC 489
Db 2558 HTISLNC 2564
```

```
RESULT 13
US-11-186-284-49
; Sequence 49, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; FILE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MEMO1-029P2RNM
; CURRENT FILING DATE: 2005-07-21
; PRIOR FILING DATE: 2005-07-21
; PRIOR FILING DATE: 2002-11-21
; PRIOR FILING DATE: 2001-12-10
; PRIOR FILING DATE: 2001-12-10
; PRIOR FILING DATE: 2002-03-05
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 2828
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-186-284-49
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Query Match 2.9%; Score 106; DB 7; Length 2828;
Best Local Similarity 22.2%; Pred. No. 0.71;
Matches 108; Conservative 56; Mismatches 157; Indels 166; Gaps 30;

QY 72 WTRQDRDLLEEFNPLPENRI-----SKEKDVLMFRPTLL-----NDTGNVTCMLR 117
Db 2175 WPR-----ILWRLPSKRMIDALFSDSRK--VFANGTLVVKSVTKDAGDYLCVAR 2224
QY 118 NTTYCSKVAPLEVVQKDCSCFNSPKMLP-----VHKLYIEYGIORITC-----PNVDGYF 167
Db 2225 NKVGDDYVVLKVDVVMK-----PAKIEHKEENDHKVFG-GDLKVDVCATGLPN----- 2272
QY 168 PSSVVPPTITWYMGCVKION-----FNNVIPEGMNLISFLIALISNNGY 210
Db 2273 -----PEISWSLPGSLVNSFMQSDSGGRTKRYVVFNN-----GTLFYFNEVGMREEGY 2322
QY 211 TCVVITYPEN--GRTHLTRLTVKVGSP---KNAPVPVIHSPNDHVVEKEPGEELLIP 265
Db 2323 TC---FAENQVGKDEMVR---VKVVTAPATIRNKTLYLAVQVPY-----GDVVTVA 2367
```

```
Qy 266 CTVYFSLMDSRNEVWWTIDGKKPDDITIDVTINESISHSRTEDETRTQILSIKKVTSED 325
Db 2368 C-----EAKGEMPKVTLWSP-----TNKVIPTSSSEKYQIYQDGT-----LLIQAQRSD 2412
Qy 326 LKRSYVCHARGAKGEVAKAAVKQKV-----PAPRYTV-ELACGFGATVLLVWL-- 374
Db 2413 -SGNYTCLVRNSAGEDRTVWVHNVPKPNPNPITTVRETAAG-GSKRLDCKAEG 2470
Qy 375 IWVHVYWL--EMVLFYRAHFGTDETDLDGKEYDIYVSYARNABEEBFVLLTLRGLVLENE 432
Db 2471 IPTPRVLWAFPEGVVLVPPAPYYGNRITVHGNSLDI-----RSLKSDSVQLVC--MARNE 2523
Qy 433 FGKLCIFDRSLPGCNTVEAFDFIQSRMIV---VLSP-----DYVTEKSIWLE 482
Db 2524 GG-----EARLIQVLTVLEPMKEPIPHDPISSEKITAMAG 2557
Qy 483 FKLGMVC 489
Db 2558 HTISLNC 2564
```

RESULT 14

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US-11-135-855-36
; Sequence 36, Application US/11135855
; Publication No. US2005025557A1
; GENERAL INFORMATION:
; APPLICANT: SMITHKLINE BEECHAM CORPORATION
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50013
; CURRENT APPLICATION NUMBER: US/11/135,855
; CURRENT FILING DATE: 2005-05-24
; PRIOR APPLICATION NUMBER: US/10/203,708
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: PCT/US01/04703
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 60/182,172
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 60/186,084
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 36
; LENGTH: 1694
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-135-855-36
```

```
Query Match 2.9%; Score 105; DB 7; Length 1694;
Best Local Similarity 20.8%; Pred. No. 0.41; Mismatches 85; Indels 80; Gaps 13;
Matches 55; Conservative 44;

Qy 108 DTGNYTCMLR-----NTTYCSKVAFPLEVYVQKDCSCFNPMKLPVHKLYIEYGIQRTCP 161
Db 1229 DEGFYSCARSPLQANTSLRLLEGVRVILAPAAV--PEGAPI-----TVTCA 1276

Qy 162 NVDGYPSSVKPTI-TWYMGCKYKIQNNVPIEG--MNLISFLIALISNNGNYTCVWTYPE 218
Db 1277 D-----PAAHAPTLYTWYHNGRWLQ-----EGPAASLSFLVATRAHAGAYSCQAQDAQ 1324

Qy 219 NGRTFHLTRLTVKVGSPKNVPPVTHSPNDHVYKEPGEELLIPCTVYVFSFLMDSRN 278
Db 1325 GTR-----SSRPAALQVLYAPQDAVL-----SSFRDSRA 1353

Qy 279 E-----VWMTIDGKKPDDITID-----VTINESISHSRTEDETRTQI-----LSIKKVTSE 324
Db 1354 RSMAVIQCTVDSEPPAEALSHDGKVLATSSGVHSLASGTGHVQVARNALRLQVDVPAG 1413

Qy 325 DLKRSYVCHARGAKGEVAKAAVK 348
Db 1414 D--DTYVCTAQNLLGSISTIGRLQ 1435
```

Search completed: December 7, 2005, 13:47:20
Job time : 15 secs

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RESULT 15
US-11-135-855-35
; Sequence 35, Application US/11135855
; Publication No. US2005025557A1
; GENERAL INFORMATION:
; APPLICANT: SMITHKLINE BEECHAM CORPORATION
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50013
; CURRENT APPLICATION NUMBER: US/11/135,855
; CURRENT FILING DATE: 2005-05-24
; PRIOR APPLICATION NUMBER: US/10/203,708
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: PCT/US01/04703
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 60/182,172
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 60/186,084
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 35
; LENGTH: 1709
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-135-855-35
```

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Query Match 2.9%; Score 105; DB 7; Length 1709;
Best Local Similarity 20.8%; Pred. No. 0.42; Mismatches 85; Indels 80; Gaps 13;
Matches 55; Conservative 44;

Qy 108 DTGNYTCMLR-----NTTYCSKVAFPLEVYVQKDCSCFNPMKLPVHKLYIEYGIQRTCP 161
Db 1229 DEGFYSCARSPLQANTSLRLLEGVRVILAPAAV--PEGAPI-----TVTCA 1276

Qy 162 NVDGYPSSVKPTI-TWYMGCKYKIQNNVPIEG--MNLISFLIALISNNGNYTCVWTYPE 218
Db 1277 D-----PAAHAPTLYTWYHNGRWLQ-----EGPAASLSFLVATRAHAGAYSCQAQDAQ 1324

Qy 219 NGRTFHLTRLTVKVGSPKNVPPVTHSPNDHVYKEPGEELLIPCTVYVFSFLMDSRN 278
Db 1325 GTR-----SSRPAALQVLYAPQDAVL-----SSFRDSRA 1353

Qy 279 E-----VWMTIDGKKPDDITID-----VTINESISHSRTEDETRTQI-----LSIKKVTSE 324
Db 1354 RSMAVIQCTVDSEPPAEALSHDGKVLATSSGVHSLASGTGHVQVARNALRLQVDVPAG 1413

Qy 325 DLKRSYVCHARGAKGEVAKAAVK 348
Db 1414 D--DTYVCTAQNLLGSISTIGRLQ 1435
```

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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 14, 2005, 11:46:30 ; Search time 322 Seconds
(without alignments)
3792.500 Million cell updates/sec

Title: US-10-061-727-2
Perfect score: 3669
Sequence: 1 MTLMLCVSLVYFIQSDA.....SALALHFTDLNNDFYIL 687

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Maximum Match 100%
Listing first 45 summaries

Post-processing: Minimum Match 0%

Command line parameters: -DEV=xlh
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-MODE=LOCAL -OUTFMT=PCO -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10061727@cgn_1_1_193@runat_07122005_113337_17228 -NCPU=6 -ICPU=3
-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA.*

1: /cgn2_6/ptodata/1/ina/1 COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5 COMB.seq.*
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4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
5: /cgn2_6/ptodata/1/ina/H COMB.seq.*
6: /cgn2_6/ptodata/1/ina/PCTUS COMB.seq.*
7: /cgn2_6/ptodata/1/ina/PP COMB.seq.*
8: /cgn2_6/ptodata/1/ina/RE COMB.seq.*
9: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2591.5	70.6	4724	3	US-09-949-016-313 Sequence 313, App
2	2591.5	70.6	4726	3	US-09-949-016-5448 Sequence 5448, Ap
3	2586	70.5	1740	3	US-08-991-944-1 Sequence 1, Appli
4	2327.5	63.4	3355	3	US-08-991-944-3 Sequence 3, Appli
5	1938	52.8	2748	3	US-10-282-162-51 Sequence 51, Appl
6	1937.5	52.8	2754	3	US-10-282-162-53 Sequence 53, Appl
7	1937.5	52.8	2754	3	US-10-282-162-55 Sequence 55, Appl
8	1935	52.7	2703	3	US-10-282-162-39 Sequence 39, Appl
9	1935	52.7	2709	3	US-10-282-162-41 Sequence 41, Appl

10	1935	52.7	2709	3	US-10-282-162-43 Sequence 43, Appl
11	1930	52.6	2733	3	US-09-313-942-27 Sequence 27, Appl
12	1930	52.6	2733	3	US-10-282-162-27 Sequence 27, Appl
13	1833	50.0	2703	3	US-10-282-162-33 Sequence 33, Appl
14	1833	50.0	2709	3	US-10-282-162-35 Sequence 35, Appl
15	1833	50.0	2709	3	US-10-282-162-37 Sequence 37, Appl
16	1830	49.9	2754	3	US-10-282-162-47 Sequence 47, Appl
17	1830	49.9	2754	3	US-10-282-162-49 Sequence 49, Appl
18	1829	49.9	2748	3	US-10-282-162-45 Sequence 45, Appl
19	825	22.5	2061	3	US-09-173-151A-3 Sequence 3, Appli
20	800	21.8	1737	3	US-09-173-151A-1 Sequence 1, Appli
21	767	20.9	2537	3	US-09-173-151A-34 Sequence 34, Appl
22	536	14.6	141454	3	US-09-949-016-12055 Sequence 12055, A
23	536	14.6	141455	3	US-09-949-016-17190 Sequence 17190, A
24	528.5	14.4	1620	3	US-08-996-338-7 Sequence 7, Appli
25	528.5	14.4	1620	3	US-09-556-972-7 Sequence 7, Appli
26	528	14.4	1626	2	US-08-604-333-1 Sequence 1, Appli
27	528	14.4	1626	3	US-09-110-618-1 Sequence 1, Appli
28	528	14.4	1626	3	US-09-578-178-1 Sequence 1, Appli
29	528	14.4	1626	3	US-09-577-806-1 Sequence 1, Appli
30	528	14.4	1626	3	US-09-621-502-3 Sequence 3, Appli
31	528	14.4	3522	3	US-09-023-655-906 Sequence 906, App
32	528	14.4	3522	3	US-09-949-002-74 Sequence 74, Appl
33	520	14.2	1563	3	US-09-949-002-203 Sequence 203, App
34	520	14.2	1563	3	US-08-996-338-1 Sequence 1, Appli
35	520	14.2	1563	3	US-09-556-972-1 Sequence 1, Appli
36	495	13.5	2314	3	US-09-173-151A-9 Sequence 9, Appli
37	495	13.5	2668	3	US-09-949-002-204 Sequence 204, App
38	495	13.5	2681	3	US-09-621-502-1 Sequence 1, Appli
39	495	13.5	2681	3	US-09-616-530A-6 Sequence 6, Appli
40	495	13.5	2681	3	US-10-212-356A-6 Sequence 6, Appli
41	495	13.5	2681	3	US-10-212-287-6 Sequence 6, Appli
42	495	13.5	2681	3	US-09-949-002-72 Sequence 72, Appl
43	488.5	13.3	2356	2	US-07-821-716-3 Sequence 3, Appli
44	484.5	13.2	1782	2	US-08-381-603-3 Sequence 3, Appli
45	484.5	13.2	1782	3	US-08-924-376-3 Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-09-949-016-313
; Sequence 313, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 313
; LENGTH: 4724
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-313

Alignment Scores:
Pred. No.: 1.16e-258 Length: 4724
Score: 2591.50 Matches: 502
Percent Similarity: 86.84% Conservative: 39
Best Local Similarity: 80.58% Mismatches: 50
Query Match: 70.63% Indels: 32
DB: 3 Gaps: 7

US-10-061-727-2 (1-687) x US-09-949-016-313 (1-4724)

Qy 1 MetThrLeuLeuTrpCysValValSerLeuTyrPheTyrGlyIleLeuGlnSerAspAla 20
Db 207 ATGACACTTCGTGGTGTAGTGAGTCTCTACCTTTATGGAAATCCGCAAGGTGATGCC 266
Qy 21 SerGluArgCysAspAspTrpGlyLeuAspThrMetArgGlnIleGlnValPheGluAsp 40
Db 267 TCAGAAACGCTCGATAGCTGGGAGCTAGACACCATGAGGCAAAATCCAAAGTGTTTGAAGAT 326
Qy 41 GluProAlaArgIleLysCysProLeuPheGluHisPheLeuLysPheAsnTyrSerThr 60
Db 327 GAGCCAGCTCGCATCAAGTGCCTCTTTGAAACACTTCTTGAATTTCAACTACAGCACA 386
Qy 61 AlaHisSerAlaGlyLeuThrLeuIleTrpTyrTrpThrArgGlnAspArgAspLeuGlu 80
Db 387 GCCCATTCAGTGGCTTACTCTGATCTGGTATTGGACTAGGCAGGACCGGCCTTGGAG 446
Qy 81 GluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTrp 100
Db 447 GAGCCAAATTAACTTCCGCTCCCGAGAACCGCATTTAGTAAGGAGAAAGATGTGCTGTGG 506
Qy 101 PheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThr 120
Db 507 TTCCGGCCCACTCTCTCAATGACACTGGCNACTATATACCTGTCATGTTAAGGAACACTACA 566
Qy 121 TyrCysSerLysValAlaPheProLeuGluValValGlnLysAspSerCysPheAsnSer 140
Db 567 TATTGCAGCAAGTTGCATTTCCCTTGGAAAGTTGTTCAAAAAGACAGCTGTTTCAATTCC 626
Qy 141 ProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArgIleThrCys 160
Db 627 CCCATGAACATCCAGTGCATAAACTGTATATAGATATATGCAATTCAGAGGATCACTTGT 686
Qy 161 ProAsnValAspGlyTyrPheProSerSerValLysProThrIleThrTrpTyrMetGly 180
Db 687 CCAAATGTAGATGATATTTCTTCCAGTGTCAACCGACTATCACTTGGTATATGGGC 746
Qy 181 CysTyrLysIleGlnAsnPheAsnAsnValIleProGluGlyMetAsnLeuSerPheLeu 200
Db 747 TGTATAAAATACAGAATTTTAAATGTAATACCCGAAGGTATGAACCTTGAGTTTCCCTC 806
Qy 201 IleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValThrTyrProGluAsnGly 220
Db 807 ATTCCCTTAAATTTCAAAATAATGGAATTTACACATGTGTGTGTATACATATCCAGAAATGGA 866
Qy 221 ArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProLysAsnAla 240
Db 867 CGTACGTTTCATCTCACAGGACTCTGACTGTAAGGTAGTAGGCTCTCCAAAATAATGCA 926
Qy 241 ValProProValIleHisSerProAsnAspHisValValTyrGluLysGluProGlyGlu 260
Db 927 GTGCCCCCTGTGATCCATTCACCTTAATGATCATGTGTCTATGAGAAAGAACCCAGGAGAG 986
Qy 261 GluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAspSerArgAsnGluVal 280
Db 987 GAGCTACTCATTCCTGTACGGTCTATTTTGTAGTTTCTGATGGATTCGCAATGAGGTT 1046
Qy 281 TrpTrpThrIleAspGlyLysLeuProAspAspIleThrIleAspValThrIleAsnGlu 300
Db 1047 TGGTGGACCAATTGATGAAAAAACCCTGATGACATCACTATTGATGTCACCATTAACGAA 1106
Qy 301 SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLysLys 320
Db 1107 AGTATAAGTCATAGACAGAGATGAAACAGAACTCAGATTTTGGACATCAAGAAA 1166
Qy 321 ValThrSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAlaLysGlyGlu 340
Db 1167 GTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTATGCTAGAGTGCACAAAGGCGAA 1226
Qy 341 ValAlaLysAlaAlaLysValLysGlnLysValProAlaProArgTyrThrValGluLeu 360
Db 1227 GTTGCCAAAGCAGCAAGGTGAAGCAGAAAGTGGCCGCTCCAAGATACAGTGGAACTG 1286

Qy 361 AlaCysGlyPheGlyAlaThrValLeuLeuValIleLeuIleValValTyrHisVal 380
Db 1287 GCTTGTGGTTTGGAGCCACAGCTCTAGTGGTGATTTCTCATTTGTGTATTACCATGTT 1346
Qy 381 TyrTrpLeuGluMetValLeuPheTyrArgAlaHisPheGlyThrAspGluThrIleLeu 400
Db 1347 TACTGGCTAGAGATGGTCTTATTTACCGGGCTCATTTTGGAAACAGATGAACCATTTTA 1406
Qy 401 AspGlyLysGluTyrAspIleTyrValSerTyrAlaArgAsnAlaGluGluGluPhe 420
Db 1407 GATGAAAACAGATGATGATATTTATGATCTCTATGCAAGGAATGCGGAAGAAGAAATTT 1466
Qy 421 ValLeuLeuThrLeuArgGlyValLeuGluAsnGluPheGlyTyrLysLeuCysIlePhe 440
Db 1467 GTATTACTGACCTCCGTGGAGTTTGGAGAATGAAATTTGGATACAAAGCTGTGCATCTTT 1526
Qy 441 AspArgAspSerLeuProGlyGlyAsnThrValGluAlaValPheAspPheIleGlnArg 460
Db 1527 GACCGAGACAGTCTGCTGGGGAAATTTGTCCACAGATGAGACTTTGAGCTTCATTTCAAAA 1586
Qy 461 SerArgArgMetIleValValLeuSerProAspTyrValThrGluLysSerIleSerMet 480
Db 1587 AGCAGACGCTCTCTGGTTGTTCTTAAGCCCCAACTACGTGCTCCAGGGAACCCAGGCCTC 1646
Qy 481 LeuGluPheLysLeuGlyValMetCysGlnAsnSerIleAlaThrLys----- 496
Db 1647 CTGGAGCTCAAGCTGGCCTA-----GAAAATATGGCTCTCGGGGCAACATCAAC 1697
Qy 497 LeuIleValValGluTyrArgProLeuGluHisProHisProGlyIleLeuGlnLeuLys 516
Db 1698 GTCATTTTAGTACAGTACAAAGCTGTGAAGGAAACGAAAG-----GTGAAGAGCTGAAG 1751
Qy 517 GluSer-----ValSerPheValSerTrpLysGlyGlyLysSerLysHisSerGly 533
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Qy 554 GlyTrpAsnGluSerCysSerSerGlnSerAspIleSerLeuAspHisVal-GlnArgAr 573
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Qy 573 GArg-----SerArgLeuLysGluProProGluLeuGlu 584
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Qy 604 YLysSer 606
Db 2022 TCTAAGC 2028

RESULT 2

; Sequence 5448, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: GL001307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 5448
 ; LENGTH: 4726
 ; TYPE: DNA
 ; ORGANISM: Human
 US-09-949-016-5448

Alignment Scores:
 Pred. No.: 1,16e-258 Length: 4726
 Score: 2591.50 Matches: 502
 Percent Similarity: 86.84% Conservative: 39
 Best Local Similarity: 80.58% Mismatches: 50
 Query Match: 70.63% Indels: 32
 DB: 3 Gaps: 7

US-10-061-727-2 (1-687) x US-09-949-016-5448 (1-4726)

QY 1 MetThrLeuLeuTrpCysValValSerLeuTyrPheTyrGlyIleLeuGlnSerAspAla 20
 DB 207 ATGACATTCCTGGTGTGTAGTCTCTACTTTTATGGAAATCCTGCNAAGTATGCC 266
 QY 21 SerGluArgCysAspAspTrpGlyLeuAspThrMetArgGlnIleGlnValPheGluAsp 40
 DB 267 TCAGAACGCTGGCATGCTGGGACTAGACACCATGAGGCAAAATCCAAGTGTTCGAAGAT 326
 QY 41 GluProAlaArgIleIleCysProLeuPheGluHisPheLeuLysPheAsnTyrSerThr 60
 DB 327 GAGCCAGCTCGCATCAAGTGGCCACTCTTTGAACACACTCTTTGAAATTCAACTACAGCACA 386
 QY 61 AlaHisSerAlaGlyLeuThrLeuIleTrpTyrTrpThrArgGlnAspArgAspLeuGlu 80
 DB 387 GCCCATTCAGCTGGCTTACTCTGATCTGGTATTGGACTAGGACGAGCCGGACCTTGAG 446
 QY 81 GluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTrp 100
 DB 447 GAGCCAAATTAACCTCCGCTCCCGAGAACCGCATTAGTAAGAGAAAGATGTGCTGTGG 506
 QY 101 PheArgProThrLeuLeuAsnAspThrGlyAsnTyrTrpCysMetLeuArgAsnThrThr 120
 DB 507 TCCCGGCCACTCTCCTCAATGACACTGGCAACTATACCTGCATGTTAAGGAACAACATA 566
 QY 121 TyrCysSerLysValAlaPheProLeuGluValValGlnLysAspSerCysPheAsnSer 140
 DB 567 TATTGCAGCAAGTTGCAATTCCTTGGAGTTGTTCAAAAAGACAGCTGTTTCAATTC 626
 QY 141 ProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArgIleThrCys 160
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 QY 161 ProAsnValAspGlyTyrPheProSerSerValLysProThrIleThrTyrMetGly 180
 DB 687 CCAATGTAGATGGATATATTTTCCATGTCACAAACCGACTATCACTTGGTATATGGGC 746
 QY 181 CysTyrLysIleGlnAsnPheAsnValIleProGluGlyMetAsnLeuSerPheLeu 200
 DB 747 TGTATAAATATACAGAAATTTAATATGTAATACCCGAGAGGTATGAATCTTGATTTCTCT 806
 QY 201 IleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValThrTyrProGluAsnGly 220
 DB 807 ATTGCTTTAAATTCAAATAATGAAATTAACACATGTGTGTGTATACATATCCAGAAATGGA 866
 QY 221 ArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProLysAsnAla 240
 DB 867 CGTACGTTTCATCTCACCAGGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAAAATGCA 926
 QY 241 ValProProValIleHisSerProAsnAspHisValValTyrGluLysGluProGlyGlu 260
 DB 927 GTGCCCTCTGTATCCATTCACCTAATGATCATGTGGTCTATGAGAAAGAACCCAGGAGAG 986
 QY 261 GluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAspSerArgAsnGluVal 280

DB 987 GAGCTACTCATTTCCCTGACGGTCTATTTTAGTTTCTGATGATTCTCGCAATGAGGTT 1046
 QY 281 TrpTrpThrIleAspGlyLysLysProAspAspIleThrIleAspValThrIleAsnGlu 300
 DB 1047 TGGTGGACCATTTGATGGAAAAAACCTGATGACATCACTATTGATGTCCACCAATTAACGAA 1106
 QY 301 SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLysLys 320
 DB 1107 AGTATAAGTCATAGTAGACAGAGATGAAACAGAACTCAGATTTTGAGCATCAAGAAA 1166
 QY 321 ValThrSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAlaLysGlyGlu 340
 DB 1167 GTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGCTAGTGTGATCTCATTTGTTTACCATGTT 1226
 QY 341 ValAlaLysAlaAlaLysValLysGlnLysValProAlaProArgTyrThrValGluLeu 360
 DB 1227 GTTGCCAAAGCAGCCCAAGGTGAAGCAGAAAGTGCAGCTCCAGATACACAGTGAACATG 1286
 QY 361 AlaCysGlyPheGlyAlaThrValLeuLeuValValIleLeuIleValValTyrHisVal 380
 DB 1287 GCTTGTGGTTTGGAGCCACAGTCTCTGCTAGTGTGATCTCATTTGTTTACCATGTT 1346
 QY 381 TyrTrpLeuGluMetValLeuPheTyrArgAlaHisPheGlyThrAspGluThrIleLeu 400
 DB 1347 TACTGGCTAGAGATGCTCTATTTTACCGGCTCATTTTGGAAACAGATGAACACATTTTA 1406
 QY 401 AspGlyLysGluTyrAspIleTyrValSerTyrAlaArgAsnAlaGluGluGluPhe 420
 DB 1407 GATGAAAGAGTATGATATTTATGTATCTTATGCAAGGAATGCGGAAGAAAGAAATTT 1466
 QY 421 ValLeuLeuThrLeuArgGlyValLeuGluAsnGluPheGlyTyrLysLeuCysIlePhe 440
 DB 1467 GTATTACTGACCTCCGCTGGAGTTTGGAGAAATGAAATTTGGATACAAAGCTGTGCATCTTT 1526
 QY 441 AspArgAspSerLeuProGlyGlyAsnThrValGluAlaValPheAspPheIleGlnArg 460
 DB 1527 GACCGAGACAGCTGCTCGCTGGGGAATTTGTACAGATGAGACTTTTGAGCTTCATTTCAGAAA 1586
 QY 461 SerArgArgMetIleValValLeuSerProAspTyrValThrGluLysSerIleSerMet 480
 DB 1587 AGCAGACGCTCTCGTGTGTTTCTAAGCCCACTACGTGCTCCAGGGAACCCCAAGCCCTC 1646
 QY 481 LeuGluPheLysLeuGlyValMetCysGlnAsnSerIleAlaThrLys 496
 DB 1647 CTGGAGCTCAAGGCTGGGCTA-----GAAATATGGCTCTCGGGGCAACATCAAC 1697
 QY 497 LeuIleValValGluTyrArgProLeuGluHisProHisProGlyIleLeuGlnLeuLys 516
 DB 1698 GTCATTTTAGTACAGTACAAAGCTGTGAAGGAAACGAAAG-----GTGAAAGAGCTGAAG 1751
 QY 517 GluSer-----ValSerPheValSerTrpLysGlyGluLysSerLysHisSerGly 533
 DB 1752 AGGCTTAAGACGGTGCACCGTCAATTAATGGAAGGGGAAAAATCCCAAGTATCCACAG 1811
 QY 534 SerLysPheTyrLysAlaLeuArgLeuAlaLeuProLeuArgSerLeuSerAlaSerSer 553
 DB 1812 GGCAGGTTCTGGAAGCAGCTGCAGTGGCCATGCAGTAGAAGAAAGTCCCGCGCGCTCT 1871
 QY 554 GlyTrpAsnGluSerCysSerSerGlnSerAspIleSerLeuAspPheHisVal-GlnArg 573
 DB 1872 AGCAGTGTAGCAGGCGCTCTCGTATTTCA-----TCTTTGAAAAATGTATGAAAGGAA 1925
 QY 573 gArg-----SerArgLeuLysGluProProGluLeuGlu 584
 DB 1926 TAATGAAAGGGTAAAAAGAACAAAGGGGTGCTCCAGGAAGAAAGAGTCCCGCCACAG----- 1980
 QY 584 nSerSerGluArgAlaAlaGlySerProProAlaProGly***MetSerLysHisArgGlu 604
 DB 1981 -----TCTTCATTCGCGAGTTTATGTTTTCATAGCAAAAAAATAATGCG 2021
 QY 604 yLysSer 606
 DB 2022 TCTAAGC 2028

RESULT 3

US-08-991-944-1
; Sequence 1, Application US/08991944
; Patent No. 6280955
; GENERAL INFORMATION:
; APPLICANT: Cao, Zhaodan
; TITLE OF INVENTION: Interleukin-1 Receptor Accessory Proteins,
; ; TITLE OF INVENTION: Nucleic Acids and Methods
; ; NUMBER OF SEQUENCES: 4
; ; CORRESPONDENCE ADDRESS:
; ; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; ; STREET: 75 DENISE DRIVE
; ; CITY: HILLSBOROUGH
; ; STATE: CALIFORNIA
; ; COUNTRY: USA
; ; ZIP: 94010
; ; COMPUTER READABLE FORM:
; ; MEDIUM TYPE: Floppy disk
; ; COMPUTER: IBM PC compatible
; ; OPERATING SYSTEM: PC-DOS/MS-DOS
; ; SOFTWARE: PatentIn Release #1.0, Version #1.30
; ; CURRENT APPLICATION DATA:
; ; APPLICATION NUMBER: US/08/991,944
; ; FILING DATE:
; ; CLASSIFICATION:
; ; ATTORNEY/AGENT INFORMATION:
; ; NAME: OSMAN, RICHARD A
; ; REGISTRATION NUMBER: 36,627
; ; REFERENCE/DOCKET NUMBER: T97-014
; ; TELECOMMUNICATION INFORMATION:
; ; TELEPHONE: (650) 343-4341
; ; TELEFAX: (650) 343-4342
; ; INFORMATION FOR SEQ ID NO: 1:
; ; SEQUENCE CHARACTERISTICS:
; ; LENGTH: 1740 base pairs
; ; TYPE: nucleic acid
; ; STRANDEDNESS: double
; ; TOPOLOGY: linear
; ; MOLECULE TYPE: cDNA
; ; FEATURE:
; ; NAME/KEY: CDS
; ; LOCATION: 10...1719
US-08-991-944-1

Alignment Scores:

Pred. No.:	7.57e-259	Length:	1740
Score:	2586.00	Matches:	488
Percent Similarity:	91.43%	Conservative:	35
Best Local Similarity:	85.31%	Mismatches:	37
Query Match:	70.48%	Indels:	12
DB:	3	Gaps:	4

US-10-061-727-2 (1-687) x US-08-991-944-1 (1-1740)

Qy	1	MetThrLeuLeuTyrCysValValSerLeuTyrPheTyrGlyIleLeuGlnSerAspAla	20
Db	10	ATGACACTTCTGTGGTGTAGTGAGTCTACTTTTATGGAATCCTGCAAGTGATGCC	69
Qy	21	SerGluArgCysAspAspTtpGlyLeuAspThrMetArgGlnIleGlnValPheGluAsp	40
Db	70	TCAGAACGCTCGGATGACTGGGGACTAGACACCATGAGGCAATCCAAAGTGTITGAAGAT	129
Qy	41	GluProAlaArgIleLysCysProLeuPheGluHisPheLeuLysPheAsnTyrSerThr	60
Db	130	GAGCCAGCTCGCATCAAGTGCCCACTCTTTGAACACTCTTGAAATTCACACTACAGACA	189
Qy	61	AlaHisSerAlaGlyLeuThrLeuIleTyrTrrPThrArgGlnAspArgAspLeuGlu	80
Db	190	GCCCATTCAGCTGCCCTTACTCTGATCTGGTATTGGACTAGGCAGGACCGGACCTTGAG	249
Qy	81	GluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTrrp	100

Db	250	GAGCCAAATTAACTTCCGCCTCCCGAGAACCGCAATTAGTAAGAGAAAGATGTGCTGTGG	309
Qy	101	PheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThr	120
Db	310	TTCCGGCCCACTCTCTCAATGACACTGGCAACTATACCTGTCATGTTTAAGGAACACATA	369
Qy	121	TyrCysSerLysValAlaPheProLeuGluValValGlnLysAspSerCysPheAsnSer	140
Db	370	TATTGCAGCAAAAGTTGCAATTTCCCTTGGAAAGTTTCCAAAAGACAGCTGTTTCAATTCC	429
Qy	141	ProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArgIleThrCys	160
Db	430	CCCATGAACCTCCAGTGCATAACTGTATATAGATATGGCAATTCAGAGATCATTGT	489
Qy	161	ProAsnValAspGlyTyrPheProSerSerValLysProThrIleThrTrrPTrMetGly	180
Db	490	CCAAATGTAGATGGATATTTTCTTCCAGTGTCAACCGACTATCACTTGGTATATGGGC	549
Qy	181	CysTyrLysIleGlnAsnAsnValIleProGluGlyMetAsnLeuSerPheLeu	200
Db	550	TGTTATAAAATACAGAAATTTTAATATGTAATACCCGAAGGTATGAACTTTGAGTTTCCCTC	609
Qy	201	IleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValThrTyrProGluAsnGly	220
Db	610	ATTGCCCTTAATTTCAAATAATGGAATACACATGTGTTGTACATATCCAGAAATATGGA	669
Qy	221	ArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProLysAsnAla	240
Db	670	CGTACGTTTTCATCTCACGAGACTCTGACTGTAAGGTAGTAGGCTCTCCCAAAAATGCA	729
Qy	241	ValProProValIleHisSerProAsnAspHisValValTyrGluLysGluProGlyGlu	260
Db	730	GTGCCCCCTGTGATCCATTACCTTAATGATCATGTGCTCTATGAGAAAGAACCAAGGAG	789
Qy	261	GluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAspSerArgAsnGluVal	280
Db	790	GAGCTACTCAATTCCTGTACGGTCTATTTTAGTTTTCTGATGGATTCTCGCAATGAGGTT	849
Qy	281	TrrPTrThrIleAspGlyLysLysProAspAspileThrIleAspValThrIleAsnGlu	300
Db	850	TGGTGGACCATTTGATGAAAAAACCTGATGACATCACTATTGATGTCACTTAACGAA	909
Qy	301	SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLys	320
Db	910	AGTATAGTCATAGTAAACAGAGATGAAACAAAGAACTCAGATTTTGGAGCATCAAGAA	969
Qy	321	ValThrSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAlaLysGlyGlu	340
Db	970	GTTACCTCTGAGGATCTCAAGCCGAGCTATGCTGTGTCATGCTAGAGTGCCTCAAGGGGAA	1029
Qy	341	ValAlaLysAlaAlaLysValLysGlnLysValProAlaProArgTyrThrValGluLeu	360
Db	1030	GTTGCCAAAGCAGCCCAAGGTGAAGCAGAAAGTGCCAGCTCCAAGATACACAGTGGAACTG	1089
Qy	361	AlaCysGlyPheGlyAlaThrValLeuLeuValValIleLeuIleValValTyrHisVal	380
Db	1090	GCTTGTGTTTGGAGCCACAGCTCTGTAGTGTGATTTCTCATTTGTGTGTACCATGTT	1149
Qy	381	TyrTrrPLeuGluMetValLeuPheTyrArgAlaHisPheGlyThrAspGluThrIleLeu	400
Db	1150	TACTGGCTAGAGATGGTCTTATTTTACCGGGCTCATTTTGGACACAGATGAACCATTTTA	1209
Qy	401	AspGlyLysGluTyrAspileTyrValSerTyrAlaArgAsnAlaGluGluGluPhe	420
Db	1210	GATGGAAAACAGATATGATATTTATGATCTCTATGCAAGGAATGCGGAAGAAAGAAATTT	1269
Qy	421	ValLeuLeuThrLeuArgGlyValLeuGluAsnGluPheGlyTyrLysLeuCysIlePhe	440
Db	1270	GTATTACTGACCTCCGTGGAGTTTGGAGAAATGAAATTTGGATACAAAGCTGTGATCTTT	1329
Qy	441	AspArgAspSerLeuProGlyGlyAsnThrValGluAlaValPheAspPheIleGlnArg	460
Db	1330	GACCGAGACAGTCTGCTCGGGGAATTTGTCACAGATGAGACTTTGACCTTCATTTCAGAA	1389

Qy	461	SerArgMetIleValLeuSerProAspTyrValThrGluLysSerIleSerMet	480
Db	1390	AGCAGACGCCTCCTGGTGTGTTCTAAGCCCAACTACGTGCTCCAGGAAACCCAGCCCTC	1449
Qy	481	LeuGluPheLysLeuGlyValMetCysGlnAsnSerIleAlaThrLys	496
Db	1450	CTGAGCTCAAGCTGCGCTA-----GAAATATGGCTCTCGGGCAACATCAAC	1500
Qy	497	LeuIleValValGluTyrArgProLeuGluHisProHisProGlyIleLeuGlnLeuLys	516
Db	1501	GTCAATTTTAGTACAGTACAAAGCTGTCAAGGAAACGAAG-----GTGAAAGAGCTCAAG	1554
Qy	517	GluSer-----ValSerPheValSerTrpLysGlyGluLysSerLysHisSerGly	533
Db	1555	AGGCTTAAGACGGTGCTACACGGTCATTAAATGGAAGGGGAAAAATCCAAGTATCCACAG	1614
Qy	534	SerLysPheTrpLysAlaLeuArgLeuAlaLeuProLeuArgSerLeuSerAlaSerSer	553
Db	1615	GGCAGGTTCTGAAGACAGCTGCAGGTGGCCATGCCAGTGAAGAAAGTCCCGCGCGTCT	1674
Qy	554	GlyTrpAsnGluSerCysSerSerGlnSerAspIle	565
Db	1675	AGCAGTCATGACGAGGGCCCTCTCGTATTTTCATCTTTG	1710

Best Local Similarity:	71.57%	Mismatches:	76
Query Match:	63.44%	Indels:	28
DB:	3	Gaps:	8
US-10-061-727-2 (1-687) x US-08-991-944-3 (1-3355)			
QY	1	MetThrLeuLeuTrpCysValValSerLeuTyrPheTyrGlyIleLeuGlnSerAspAla	20
DB	135	ATGGGACTTCTGTGGTATTTGATGAGTCTGTCTTCTATGGATCCTCGAGAGTCATGCT	194
QY	21	SerGluArgCysAspAspTyrGlyLeuAspThrMetArgGlnIleGlnValPheGluAsp	40
DB	195	TCGGAGCCCTGTGATGACTGGGACTAGATACCATCGCACAAATCCAAGTGTTTGAAAGT	254
QY	41	GluProAlaArgIleLysCysProLeuPheGluHisPheLeuLysPheAsnTyrSerThr	60
DB	255	GAGCCGGCTCGAATCAAGTCGCCCTCTTTGAACACATTCCTTGAAGTACAACATACAGCACT	314
QY	61	AlaHisSerAlaGlyLeuThrLeuIleTyrTrpThrArgGlnAspArgAspLeuGlu	80
DB	315	GCCCATTTCTCTGGCCTTACCTCTGATCTGTGACTGGACAGCAGACCGGACCTGGAG	374
QY	81	GluProIleAenPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTrp	100
DB	375	GAGCCCATTAATCTTCGGCTCCCAAGAAATCGCATCAGTAGGAGAAAGATGTGCTCTGG	434
QY	101	PheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThr	120
DB	435	TTCCGGCCACCCTCCTCAATGACACAGGCAATTTACACCTGCATGTTTGAGGAAACACACT	494
QY	121	TyrCysSerLysValAlaPheProLeuGluValValGlnLysAspSerCysPheAsnSer	140
DB	495	TACTGTCAGCAAAAGTTGCAATTTCCCTCGAAGTTGTTCAGAAAGGACAGCTGTTTCAATTCT	554
QY	141	ProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArgIleThrCys	160
DB	555	GCCATGAGATTCCAGTGTCACAAAGTATATTAAGCATTCATCAATGATCACATGT	614
QY	161	ProAsnValAspGlyTyrPheProSerSerValLysProThrIleThrTyrTyrMetGly	180
DB	615	CCAAATGTAGACGATACTTTCCTTCAGTGTCAAAACATCCGTCACCTTGGTATAAGGGT	674
QY	181	CysTyrLysIleGlnAenPheAsnAsnValIleProGluGlyMetAsnLeuSerPheLeu	200
DB	675	TGTACTGAAATAGTGGACTTTCATAATGTACTACCCGAGGCGATGAACCTTGAGCTTTTC	734
QY	201	IleAlaIleLysSerAenAsnGlyAsnTyrThrCysValValThrTyrProGluAsnGly	220
DB	735	ATCCCCCTGGTTTCAAAATAACGGAATTTACACATGTGTGTGTACATATCTCTGAAACCGGA	794
QY	221	ArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProLysAsnAla	240
DB	795	CGTCTCTTTTACCTCACAGACTGTGACTGTAAAGGTGTGGGCTTACCANAAGATGCA	854
QY	241	ValProProValIleHisSerProAsnAspHisValValTyrGluLysGluProGlyGlu	260
DB	855	TTGCCACCCAGATCTATTTCCAAATGACCGTGTGTCTATGAGAAAGAACACGAGAG	914
QY	261	GluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAspSerArgAsnGluVal	280
DB	915	GAACTGGTTATTCCCTCAAAAGTCTATTTCAGTTTTCATTATGGACTCTCCCAATGAGTCT	974
QY	281	TrpTrpThrIleAspGlyLysLysProAspAspIleThrIleAspValThrIleAsnGlu	300
DB	975	TGTGGACCAATTGATGGAAGAAGACCTTGATGACGTACAGTCGACATCCTATTATTAAGAA	1034
QY	301	SerIleSerHisArgThrGluAspGluThrArgThrGlnIleLeuSerIleLysLys	320
DB	1035	AGTGTAAGTTATCTTCAACGGAAGATGAACAAGGACTCAGATTTTGGACATCAACGAA	1094
QY	321	ValThrSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAlaLysGlyGlu	340
DB	1095	GTCAACCCGAGGATCTCAGCGCAACTATGTCTGTCTGTCATGCTCGAAATACCAAGGGGAA	1154

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QY 341 ValAlaLysAlaAlaLysValLysGlnLysValProAlaProArgTyrThrValGluLeu 360
Db 1155 GCTGAGCAGGCTGCCAAGGTGAACAGAAAGTATACACCAAGGTACACAGTAGAAGTCTC 1214
QY 361 AlaCysGlyPheGlyAlaThrValLeuLeuValValLysLeuValValLysValValLysVal 380
Db 1215 GCCTGTGGTTTGGAGCCAGGCTCTTCTGTGTAGTGGTCTCATTTGGTTTACCATGTT 1274
QY 381 TyrTrpLeuGluMetValLeuPheTyrArgAlaHisPheGlyThrAspGluThrIleLeu 400
Db 1275 TACTGGCTGGAGATGGTCTCTTTTACCGAGCTCACATTGGAAACAGATGAACAATCTT 1334
QY 401 AspGlyLysGluTyrAspIleTyrValSerTyrAlaArgAsnAlaGluGluGluPhe 420
Db 1335 GATGGAAGGAGTATGATATTTATGTTCTTCATCAAGAAATGGGAAGAGAGAAATTT 1394
QY 421 ValLeuLeuThrLeuArgGlyValLeuGluAsnGluPheGlyTyrLysLeuCysIlePhe 440
Db 1395 GTGCTGTGAGCTGCGTGGAGTTTGGAGNATGAGTTTGGATACAAAGCTGTGCATCTTC 1454
QY 441 AspArgAspSerLeuProGlyGlyAsnThrValGluAlaValPheAspPheIleGlnArg 460
Db 1455 GACAGACAGACGCTGCGCTGGGGAAATGTACAGATGAGAGCCCTGAGCTTCATTGAGAAA 1514
QY 461 SerArgArgMetIleValLeuSerProAspTyrValThrGluLysSerIleSerMet 480
Db 1515 AGCAGACGACTCCCTGGTGTCTTAAGTCCCAACTACGTCTCCAGGAAACACAAAGCCCTC 1574
QY 481 LeuGluPheLysLeuGlyValMetCysGlnAsnSerIleAlaThrLys----- 496
Db 1575 CTGGAGCTCAAGGCTGGCCTA-----GAAATATGCGCTCCCGGGGCAACATCAAC 1625
QY 497 LeuIleValValGluTyrArgProLeuGluHisProHisProGlyIleLeuGlnLys 516
Db 1626 GTCAATTTAGTGCAAGTACAAAGCTGTCAAGACATGAAG-----GTGAAAGAGCTGAAG 1679
QY 517 GluSer-----ValSerPheValSerTrpLysGlyGluLysSerLysHisSerGly 533
Db 1680 CGGCTGAAGCAGGTGCTCAGCGTCAATTAATGGAAGGAGAGAAATCCAAGTATCTTCAG 1739
QY 534 SerLysPheTrpLysAlaLeuArgLeuAlaLeuProLeuArgSerLeuSerAlaSerSer 553
Db 1740 GGCAGGTTCTGGAAGCAGTTGCAGGTGCCATGCCAGTGAAGAG-----AGTCCC 1790
QY 554 GlyTrpAsnGluSerCysSerSerGlnSerAspIleSerLeuAspHisValGlnArgArg 573
Db 1791 AGTGGTCT-----AGCAATGACAAGCAGGG-TCTCTCTACTCATCCCTGMAAAA 1840
QY 574 ArgSerArgLeuLysGluProProGluLeuGlnSerSerGluArgAlaAlaGlySer--- 592
Db 1841 CGTATGAAA-----GGAGAAGTGAGGGGGGTACAAAGAACACAGCGGTTCATGG 1888
QY 593 -----ProProAla-ProGly***MetSerLysHisArgGlyLysSerSer 607
Db 1889 GAGGAAGGGCCCTCTCTTCTTAGGCTGTGGCTTCATAGACAGAAAAGAGT 1943

RESULT 5
US-10-282-162-51
; Sequence 51, Application US/10282162
; Patent No. 6927044
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE OF INVENTION: AND USING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282,162
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
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; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 51
; LENGTH: 2748
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-282-162-51

Alignment Scores:
Pred. No.: 5,47e-191 Length: 2748
Score: 1938.00 Matches: 432
Percent Similarity: 63.42% Conservat: 50
Best Local Similarity: 56.84% Mismatches: 141
Query Match: 52.82% Indels: 140
DB: 3 Gaps: 19

US-10-061-727-2 (1-687) x US-10-282-162-51 (1-2748)
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QY 1 MetThrLeuLeuTrpCysValValSerLeuTyrPheTyrGlyIleLeuGlnSerAspAla 20
Db 1 ATGGTGGTCTCTGTGGTGTGTAGTGTCTCTCTTTTATGGAATCTCTGCAAAAGTATGCC 60
QY 21 SerGluArgCysAspAspTrpGlyLeuAspThrMetArgGlnIleGlnValPheGluAsp 40
Db 61 TCAGAACGCTGCGATGACTGGGACTAGACACCATGAGGCAAAATCCAAGTGTTTGAAGAT 120
QY 41 GluProAlaArgIleLysCysProLeuPheGluHisPheLeuLysPheAsnTyrSerThr 60
Db 121 GAGCCAGCTCGCATCAAGTGCCCACTCTTTTGAACACTCTTGTGAATTTCAACATACAGACA 180
QY 61 AlaHisSerAlaGlyLeuThrLeuIleTrpTyrTrpThrArgGlnAspArgAspLeuGlu 80
Db 181 GCCCATTCAGCTGGCTTACTCTGATCTGGTATTGGACTAGGACGACCGGACCTTGAG 240
QY 81 GluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTrp 100
Db 241 GAGCCAAATAACTTCCGCTCCCGAGAACCGCATTAGTAAGGAGAAAGATGTGCTGTGG 300
QY 101 PheArgProThrLeuLeuAsnAspThrGlyAsnTyrTrpCysMetLeuArgAsnThrThr 120
Db 301 TTCGGGCCCACTCTCTCAATGACACTGCGCACTATACCTGTCATGTGTTAAGGAAACACTACA 360
QY 121 TyrCysSerLysValAlaPheProLeuGluValValGlnLysAspSerCysPheAsnSer 140
Db 361 TATTGAGCAAAAGTTGCATTTCCCTTGGAAAGTTGTTCAAAAAGACAGCTGTTTCAATTC 420
QY 141 ProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArgIleThrCys 160
Db 421 CCCATGAAACTCCCGAGTGCATAAACTGTATATAGAATATGGCATTCAGAGGATCCTTGT 480
QY 161 ProAsnValAspGlyTyrPheProSerSerValLysProThrIleThrTrpTyrMetGly 180
Db 481 CCAAAATGTATAGATGGATATTTTCTCCAGTGTCAAAACCGACTATCACTTGTGTATGGGC 540
QY 181 CysTyrLysIleGlnAsnPheAsnValIleProGluGlyMetAsnLeuSerPheLeu 200
Db 541 TGTTATAAATAACAGAAATTTTAAATATGTAATACCCGGAAGGTATGAACCTTGAGTTTCTC 600
QY 201 IleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValThrTyrProGluAsnGly 220
Db 601 ATTGCCCTTAATTTCAAAATAAATAATACACATGTGTGTTTACATATCCAGAAAAATGGA 660
QY 221 ArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProLysAsnAla 240
Db 661 CGTACCTTTTCATCTCACCGAGACTCTGACTGTAAAGGTAGTAGGCTCTTCCAAAAATGCA 720
QY 241 ValProProValIleHisSerProAsnAspHisValValTyrGluLysGluProGlyGlu 260
Db 721 GTGCCCTCTGTGATCCATTACCTAATGATCATGTGGTCTATGAGAAAGAACCCAGGAGAG 780
QY 261 GluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAspSerArgAsnGluVal 280
Db 781 GAGTACTCATTCCTGTCAGGCTATTTTAGTTTCTGTAGTGTCTCTCGCAATGAGGTT 840
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QY 281 TrpTrpThrIleAspGlyLysProAspAspIleThrIleAspValThrIleAsnGlu 300
DB 841 TGGTGGACCATTTGATGGAAAAAACCCTGATGACATCACTATTGATGTACCAATTACGNA 900
QY 301 SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLys 320
DB 901 AGTATAAGTCATAGTAGAACAAGATGAACAAGAACTCAGATTTTGAGCATCAAGAA 960
QY 321 ValThrSerGluAspLeuLysArgSerTyValCysHisAlaArgSerAlaLysGlu 340
DB 961 GTTACCTCTGAGATCTCAAGCGCAGCTATGCTGTGTCATGCTAGAGTGCCAAAGCGGAA 1020
QY 341 ValAlaLysAlaAlaLysValLysGlnLysValProAlaProArgTyThrValGluLeu 360
DB 1021 GTTCCCAAGCAGCAGGAGGAGCAGAAAGTGCCAGCTCCAAAGATACACAGTGCACACA 1080
QY 361 -----AlaCysGlyPhe----- 364
DB 1081 GGGGCTGCCAGAAGCTGCCGGTTTCGTGGGAGGCATTACAAGGGGAGTTCAGGGCTGGAA 1140
QY 365 GlyAlaThrValLeuLeuValValIleLeuIleValValTyHisValTyTrpLeuGlu 384
DB 1141 GGGGAGCCTGTAGCCCTGAGGTGCCCCAGGTG-----CCCTACTGTTGTGG 1188
QY 385 MetValLeuPheTyArgAlaHisPhe----- 393
DB 1189 GCCTCTGTCAGCCCGCATCAACCTGACATGCATGATCAATAAATGACTCTGCTAGGAGGTC 1248
QY 394 ---GlyThrAspGluThrIleLeuAspGlyLysGluTyAspIleTyValSerTyAla 412
DB 1249 CCAGGAGAAGAAGACACGGATGTGGGCCAGGAGGTCTGTGGCTTCTGCCAGCC 1308
QY 413 ArgAsnAlaGluGluGluPheValLeuLeuLeuThrLeuArgGlyValLeuGluAsnGlu 432
DB 1309 TTGCGAGGAGGACTCTGGCACCTACGCTGCTGCACTACTAGAAATGCTTCTTACTGTGACAAA 1368
QY 433 PheGlyTyLysLeuCysIlePheAspArgAspSerLeuProGlyGlyAsnThrValGlu 452
DB 1369 ATGTCATTGACCTAGAGTTTGTAG-----AATACA---GAT 1404
QY 453 AlaValPheAspPheIleGlnArgSerArgMetIle-----ValVal 467
DB 1405 GCTTCTCTCCGCTCATCTCATACCGCAAAATTTTAACTTGTCAACCTCTGGGGTATTA 1464
QY 468 LeuSerProAspTyValThrGluLysSerIleSerMetLeuGluPheLysLeuGlyVal 487
DB 1465 GTATGCCCTGAC-----CTGAGTGAATTC----- 1488
QY 488 MetCysGlnAsnSerIleAlaThrLysLeuIleValValGluTyArgProLeuGluHis 507
DB 1489 -----ACCGTGACAAAACCTGACGTGAAGATTCAATGGTACAAG----- 1527
QY 508 ProHisProGlyIleLeuGlnLysGluSerValSerPheValSerTrpLysGlyGlu 527
DB 1528 -----GATTCCTCTTTTGGATAAAGACATGAGAAATTTCTAAGTGTGAGGGGACC 1581
QY 528 LysSer----- 529
DB 1582 ACTCACTTACTCGTACAGATGTGGCCCTGGGAAGATGTGGCTATTACCGCTGTGCTCGT 1641
QY 530 -----LysHisSerGlySerLysPhe-----TrpLysAlaLeuArgLeuAlaLeu--- 544
DB 1642 ACATTGGCCCATGAAGGGCAGCAATACACATCACTAGGAGTATTGAGCTAGCATCAAG 1701
QY 545 -----ProLeuArgSerLeuSerAlaSer 552
DB 1702 AAAAAAAGAGAGACCATTCCTGTGATCATTTCCCCCTCAAGACCATATCAGCTTCT 1761
QY 553 SerGlyTrpAsnGluSerCysSerSerGlnSerAspIleSerLeuAspHisValGlnArg 572
DB 1762 CTGGGG-----TCAAG-ACTGACAATCCCATGTAAGGTGTTTCTGGG 1802
QY 573 ArgArgSerArgLeuLysGluProProGluLeuGlnSerSer-----Glu 587
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DB 1803 AACCGGCACACCTTTAACCAACCACCATGCTGTGGTGGACGCCAATGACACCCACATAGAG 1862
QY 588 ArgAlaAlaGlySerPro-----ProAlaProGly*--MetSerLys----- 601
DB 1863 GCCTTACCGGGAGCGCGTACCGAGGGGCGCACCGAGGAATATTTCAGAAAAAATATGA 1922
QY 602 -----HisArgGlyLysSerSerAla 608
DB 1923 GAATACATTTGAAGTGCCATTGATTTTGTATCCTGTGTCAAGAGAGGATTTGCACATGA 1982
QY 609 ThrCysArgCysValThrTyCysGluGlyGluAsnHisLeuArgAsnLysSerArg 628
DB 1983 TTTTAAATGTGTGTGCATAATACCTGAGTT-TTCAGACACTACGCACCCAGTCAAGG 2041
QY 629 AlaGluIleHisAsnGlnProGlnTrpGluThrHisLeuCysLysLysProValProGlnGlu 648
DB 2042 AAGCTCTCCACGTTCTCCGGAGAC-AAAACTCACATGCCACCGTGCACGACCT 2100
QY 649 SerGluThrGlnTrpIleGlnAsnGlyThrArg-----LeuGluProProAlaProGln 666
DB 2101 GAA-----CTCCTGGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCCCAAG 2148

RESULT 6
; US-10-282-162-53
; Sequence 53, Application US/10282162
; Patent No. 6927044
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; TITLE OF INVENTION: AND USING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282,162
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 53
; LENGTH: 2754
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-282-162-53

Alignment Scores:
Pred. No.: 6,19e-191 Length: 2754
Score: 1937,50 Matches: 432
Percent Similarity: 62.06% Conservative: 49
Best Local Similarity: 55.74% Mismatches: 135
Query Match: 52.81% Indels: 161
DB: 3 Gaps: 20

US-10-061-727-2 (1-687) x US-10-282-162-53 (1-2754)

QY 1 MetThrLeuLeuTrpCysValValSerLeuTyPheTyGlyIleLeuGlnSerAspAla 20
DB 1 ATGGTGTCTTCTGTGTGTAGTGTCTCTACTTTTATGGAATCTCTGCAAGATGATGCC 60
QY 21 SerGluArgCysAspAspTrpGlyLeuAspThrMetArgGlnIleGlnValPheGluAsp 40
DB 61 TCAGAACGCTCGATGACTGGGGACTAGACACCATGAGGCAAAATCCAAGTGTTTGAAGAT 120
QY 41 GluProAlaArgIleLysCysProLeuPheGluHisPheLeuLysPheAsnTySerThr 60
DB 121 GAGCAGCCTCGATCAAGTGCCTACTCTTTGAACACTCTTGAATTCACACTACAGCACA 180
QY 61 AlaHisSerAlaGlyLeuThrLeuIleTyTrpThrArgGlnAspArgAspLeuGlu 80
DB 181 GCCCATTGAGTGGCTTACTCTGATCTGTTGAGTATGAGTATGAGCAGGACCGGACCTTGG 240
QY 81 GluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTrp 100
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Db 241 GAGCCAAATACTCCGCTCCCGAGAACCGCAATTAGTAAGGAGAAAGATGTGCTGGG 300
Qy 101 PheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThr 120
Db 301 TTCGGGCCCACTCTCCTCAATGACACTGGCAACTATACCTGCATGTTAAAGGAACACTACA 360
Qy 121 TyrCysSerLysValAlaPheProLeuGluValValGlnLysAspSerCysPheAsnSer 140
Db 361 TATTGCAAGCAAGTTGCATTTCCCTTGGAAAGTTGTTCAAAAAGACAGCTGTTCAATTCC 420
Qy 141 ProMetLysLeuProValHisLysLeuTyrLysGluTyrGlyLysGlnArgLysThrCys 160
Db 421 CCCATGAACCTCCAGTCAGCATAACTGATATAGAAATATGCAATTCAGAGATCACCTGT 480
Qy 161 ProAsnValAspGlyTyrPheProSerSerValLysProThrLysThrTrpTyrMetGly 180
Db 481 CCAAAATGTAGATGATATTTTCTCCAGTGTCAAACCGACTATACCTTGGTATATGGGC 540
Qy 181 CysTyrLysLysGlnAsnAsnValLysProGluGlyMetAsnLeuSerPheLeu 200
Db 541 TGTATATAAATACAGAAATTTTAATAATGTAATATACCCGAAGGTATGAACCTTGAGTTCC 600
Qy 201 IleAlaLeuLeuSerAsnAsnGlyAsnTyrThrCysValValThrTyrProGluAsnGly 220
Db 601 ATTGCCTTAATTTCAATATATGGAATATACATGTGTTGTATCATATCCAGAAATATGGA 660
Qy 221 ArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProLysAsnAla 240
Db 661 CGTAGCTTTCATCTCACAGGACTCTGACTGAAGGTAGTAGGCTCTCCAAAAAATGCA 720
Qy 241 ValProProValLysHisSerProAsnAspHisValValTyrGluLysGluProGlyGlu 260
Db 721 GTGCCCCCTGTGATGCCAATTCACCTTAATGATCATGTGTTATGAGAAAGAACCAAGGAG 780
Qy 261 GluLeuLeuLeuProCysThrValTyrPheSerPheLeuMetAspSerArgAsnGluVal 280
Db 781 GAGCTACTCATCTCCTGTACCGTCTATTTAGTTTCTGATGGATTCGCAATGAGGTT 840
Qy 281 TrpTrpThrLysAspGlyLysLysProAspAspLysThrLysAspValThrLysAsnGlu 300
Db 841 TGGTGGACCAATTGATGAAAAAACCTGATGACATCACTATTGATGTCACCATTAACGAA 900
Qy 301 SerLysSerHisSerArgThrGluAspGluThrArgThrGlnLysLeuSerLysLys 320
Db 901 AGTATAAGTCATAGTAGACAGAGATGAACAGAACTGCAAGAACTCAGATTTTGGACATCA 960
Qy 321 ValThrSerGluAspLeuLysValTyrValCysHisAlaArgSerAlaLysGlyGlu 340
Db 961 GTTACCTCTGAGGATCTCAAGCGCAGCTATGTCGTCTGATGATGAGTGCACAAAGGGAA 1020
Qy 341 ValAlaLysAlaLysValLysGlnLysValProAlaProArgTyrThrValGluLeu 360
Db 1021 GTTGCCAAAGCAGCAAGGTGAAGCAGAAAGTGCCAGCTCCAGATACACAGTGCACACA 1080
Qy 361 -----AlaCysGlyPhe----- 364
Db 1081 GGGGCTGCCAAGAGCTCCGGTTTTCGTGGGAGGCATTACAAGCGGGAGTTTCAGGCTGGAA 1140
Qy 365 GlyAlaThrValLeuLeuValValLysLeuValValTyrHisValTyrTrpLeuGlu 384
Db 1141 GGGGAGCTGTAGCCCTGAGGTGCCCGCCAGGTG-----CCCTAGCTGGTTGTGG 1188
Qy 385 MetValLeuPheTyrArgAlaHisPhe----- 393
Db 1189 GCCTCTGTACGCCCGCCGATCAACCTTGACATGGCATAAAAATGACTCTGTGCTAGGACGGTC 1248
Qy 394 ---GlyThrAspGluThrLysLeuAspGlyLysGluTyrAspLysTyrValSerTyrAla 412
Db 1249 CCAGGAGAAAGACAGACAGGATGTGGGCCCGAGGCGGTCTCTGTGGCTTCTGCCAGCC 1308
Qy 413 ArgAsnAlaGluGluGluGluPheValLeuLeuLeuLeuArgGlyValLeuGluAsnGlu 432

Db 1309 TTGCAGAGAGAGACTCTGGCAGCACTACGCTGTGCACCTACTAGAAATGCTTCTTACTGTGACAAA 1368
Qy 433 PheGlyTyrLysLeuCysIlePheAspArgAspSerLeuProGlyGlyAsnThrValGlu 452
Db 1369 ATGTCCATTGAGCTCAGAGTTTTTTAG-----AATACA---CAT 1404
Qy 453 AlaValPheAspPheIleGlnArgSerArgArgMetIle-----ValVal 467
Db 1405 GCITTCCTGCGGTTTCATCTCATACCCGCAAAATTTTAACCTTGTCAACCTCTGGGGTATTA 1464
Qy 468 LeuSerProAspTyrValThrGluLysSerLysMetLeuGluPheLysLeuGlyVal 487
Db 1465 GTATGCCCTGCAC-----CTGAGTGAATTC----- 1489
Qy 488 MetCysGlnAsnSerIleAlaThrLysLeuIleValValGluTyrArgProLeuGluHis 507
Db 1489 -----ACCCGTGACAAAACCTGACGTGAGATTTCAATGGTACAG----- 1527
Qy 508 ProHisProGlyLysLeuGlnLysLeuLysGluSerValSerPheValSerTrpLysGlyGlu 527
Db 1528 -----GATTCTCTCTTTTGGATAAAGACAATGAGAAATTTCTAAGTGTGAGGGGACC 1581
Qy 528 LysSer----- 529
Db 1582 ACTCACTTACTCTGACAGATGTGGCCCTGGAAGATGCTGGCTATTACCGCTGTGCTGTG 1641
Qy 530 -----LysHisSerGlySerLysPhe-----TrpLysAlaLeuArgLeuAlaLeu--- 544
Db 1642 ACATTGCCCCATGAAGCCAGCAATACAACTACTAGTAGGATTTAGACTACGCATCAAG 1701
Qy 545 -----ProLeuArgSerLeuSerAlaSer 552
Db 1702 AAAAAAAGAGAGACCAATTCCTGTGATCATTTCCCTCCCTCAAGACCATATACGTTCT 1761
Qy 553 SerGlyTrpAsnGluSerCysSerGlnSerAspLysSerLeuAspHisValGlnArg 572
Db 1762 CTGGGG-----TCAAG-ACTGACAATCCCATGTAAGTGTGTTCTGGG 1802
Qy 573 ArgArgSerArgLeuLysGluProGluLeuGlnSerSer-----Glu 587
Db 1803 AACCGGCACACCCCTTAACCAACCATGCTGTGTGGACGGCCCAATGACACCCACATAGAGAG 1862
Qy 588 ArgAlaAlaGlySerPro-----ProAlaProGly***MetSerLys----- 601
Db 1863 CGCCTACCCGGGAGCGCGTGCAGCGGGGCCCGCAGGAAATATTCAGAAAAATAATGA 1922
Qy 602 -----HisArgGlyLysSerSerAla 608
Db 1923 GAACCTACATTGAAGTGCATGATTTTGTGATCTCTGTCAAGAGAGAGATTTGCACATGGA 1982
Qy 609 ThrCysArgCysCysValThrTyrCysGluGlyGluAsnHisLeuArgAsnLysSerArg 628
Db 1983 TTTTAAATGTGTTGTCCATAATACCTCGAGTT--TTCAGACACTACGCCACCACTCAAGG 2041
Qy 629 AlaGluIleHisAsnGlnProGlnTrpGluThrHisLeuCysLysProValProGlnGlu 648
Db 2042 -----AAGCCTCTCCACGT--- 2056
Qy 649 SerGluThrGlnTrpIleGlnAsnGlyThrArgLeuGluProAlaProGlnLysSer 668
Db 2057 -----TCTCCGAGAGATCCAAATACGGTC 2080
Qy 669 AlaLeuAlaLeuHisHisPheThrAspLeuSerAsnAsnAsp 683
Db 2081 CGCCATGCC---CATCATCCCGACCACTGAGTTCCTGGGGGGAC 2122

RESULT 7

US-10-282-162-55

; Sequence 55, Application US/10282162

; Patent No. 6927044

; GENERAL INFORMATION:

; APPLICANT: REGENERON PHARMACEUTICALS, INC.

; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING

```

; TITLE OF INVENTION: AND USING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282,162
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 55
; LENGTH: 2754
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-282-162-55

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Alignment Scores:

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Pred. No.: 6,19e-191 Length: 2754
Score: 1937.50 Matches: 432
Percent Similarity: 62.06% Conservative: 49
Best Local Similarity: 55.74% Mismatches: 135
Query Match: 52.81% Indels: 161
DB: 3 Gaps: 20

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US-10-061-727-2 (1-687) x US-10-282-162-55 (1-2754)

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Qy 1 MetThrLeuLeuTrpCysValValSerLeuTyrPheTyrGlyLeuGlnSerAspAla 20
Db 1 ATGGTCTTCTGGTGTGTAGTAGTCTCTACTTTTATGGAATCCTGCAAGTAGTATGCC 60

Qy 21 SerGluArgCysAspAspTrpGlyLeuAspThrMetArgGlnIleGlnValPheGluAsp 40
Db 61 TCAGAACGCTGCGATGACTGGGGACTAGACACCATGAGGCAATCCAAAGTGTTCAGAT 120

Qy 41 GluProAlaArgIleLysCysProLeuPheGluHisPheLeuLysPheAsnTyrSerThr 60
Db 121 GAGCCAGCTCGCATCAAGTGGCCACTTTTGAACACTTCTTGAAATTCAACTACAGCACA 180

Qy 61 AlaHisSerAlaGlyLeuThrLeuIleTrpTyrTrpThrArgGlnAspArgAspLeuGlu 80
Db 181 GCCCATTTAGCTGGCTTACTCTGATCTGGTATTGAGCTAGGACGAGCCGGACCTTGAG 240

Qy 81 GluProIleAsnPheArgLeuProGluAsnArgIleSerLysGlyLeuAspValLeuTrp 100
Db 241 GAGCCAAATTAATCTCCGCTCCCGAGAACCGCATTAGTAGGAGAAAGATGTGCTGTGG 300

Qy 101 PheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThr 120
Db 301 TTCCGGCCCACTCTCCTCAATGACACTGGCACTATACCTGCATGTTTAAAGGAACACTACA 360

Qy 121 TyrCysSerLysValAlaPheProLeuGluValValGlnLysAspSerCysPheAsnSer 140
Db 361 TATTGAGCAAGATTGGCATTTCCCTTGGAAATGTTTCAAAAAGACAGCTGTTTCAATTCC 420

Qy 141 ProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArgIleThrCys 160
Db 421 CCCATGAAATCCCAAGTCGATAAACTGTATATAGATATGGCAATTCAGAGGATCACTTGT 480

Qy 161 ProAsnValAspGlyTyrPheProSerSerValLysProThrIleThrTrpTyrMetGly 180
Db 481 CCAAAATAGATGGATATTTTCTTCCAGTGTCAAAACCGACTATCACTTGGTATATGGGC 540

Qy 181 CysTyrLysIleGlnAsnPheAsnValIleProGluGlyMetAsnLeuSerPheLeu 200
Db 541 TGTATATAAAATACAGAAATTTTAAATATGTAATACCCGGAAGGTATGAATCTGAGTTTCTC 600

Qy 201 IleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValThrTyrProGluAsnGly 220
Db 601 ATTGCTTAAATTTCAAAATATGGAATTTACACATGTGTTGTATACATATCCAGAAAATGGA 660

Qy 221 ArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProLysAsnAla 240
Db 661 CGTAGTTTTCATCTCACCAGGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAATAATGCA 720

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Qy 241 ValProValIleHisSerProAsnAspHisValValTyrGluLysGluProGlyGlu 260
Db 721 GTGCCCCCTGTGATCCATTCACCTAATGATCATGTGGTCTATGAGAAAGAACAGAGAG 780

Qy 261 GluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAspSerArgAsnGluVal 280
Db 781 GAGCTACTCATTTCCCTGTACGGTCTATTTTAGTTTCTGTAGTATTCGCAATGAGGTT 840

Qy 281 TrpTrpThrIleAspGlyLysLysProAspAspIleThrIleAspValThrIleAsnGlu 300
Db 841 TGGTGGACCATTTGATGGAAAAAACCTCATGACATCACTATTATGATGTCCCAATTAACGAA 900

Qy 301 SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLysLys 320
Db 901 AGTATAGTCATAGTAGAACAGAGATGAAACAGNACTCAGATTTTGAGCATCAGAA 960

Qy 321 ValThrSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAlaLysGlyGlu 340
Db 961 GTTACCTCTGAGGATCTCAAGCGCAGCTATGCTGTCATGCTAGAGTGCACAAAGCGAA 1020

Qy 341 ValAlaLysAlaAlaLysValLysGlnLysValProAlaProArgTyrThrValGluLeu 360
Db 1021 GTTCCAAAGCAGCCAGGTGAAGCAGAAAGTGCAGCTCCAAGATACACAGTGCACACA 1080

Qy 361 -----AlaCysGlyPhe----- 364
Db 1081 GGGGCTGCCAAGAGCTGCCGGTTTCGTGGGAGGCAATTACAAGCGGAGTTCAGGCTGAAA 1140

Qy 365 GlyAlaThrValLeuLeuValIleLeuIleValValTyrHisValTyrTrpLeuGlu 384
Db 1141 GGGGAGCGCTGTAGCCCTGAGGTGCCCGCAGGTG-----CCCTACTGTTGTGG 1188

Qy 385 MetValLeuPheTyrArgAlaHisPhe----- 393
Db 1189 GCCTCTGTGACCCCGCGCATCAACCTGACATGGCATATAAAATGACTCTGCTAGGACGGTC 1248

Qy 394 --GlyThrAspGluThrIleLeuAspGlyLysGluTyrAspIleTyrValSerTyrAla 412
Db 1249 CCAGAGAGAGAGACACGGATGTGGGCCGAGCAGCGTCTGTGTGCTCTGTCAGGCC 1308

Qy 413 ArgAsnAlaGluGluGluGluPheValLeuLeuThrLeuArgGlyValLeuGluAsnGlu 432
Db 1309 TTGCAGGAGGACTCTGGCACCTCGTCTGCACACTAGAAATGCTTCTTACTGTGCACAAA 1368

Qy 433 PheGlyTyrLysLeuCysIlePheAspArgAspSerLeuProGlyGlyAsnThrValGlu 452
Db 1369 ATGTCCATTGAGCTCAGAGTTTGTGAG-----AATACA---GAT 1404

Qy 453 AlaValPheAspPheIleGlnArgSerArgMetIle-----ValVal 467
Db 1405 GCTTTCCTGCGGTCATCTCATACCGCAATTTTAACTTGTCACTCTGGGGTATTA 1464

Qy 468 LeuSerProAspTyrValThrGluLysSerIleSerMetLeuGluPheLysLeuGlyVal 487
Db 1465 GTATGCCCTGAC-----CTGAGTGAATTC----- 1488

Qy 488 MetCysGlnAsnSerIleAlaThrLysLeuIleValValGluTyrArgProLeuGluHis 507
Db 1489 -----ACCCGTCGAAAACTCAGCTGAAGATTTCAATGGTACAAAG----- 1527

Qy 508 ProHisProGlyIleLeuGlnLeuLysLeuSerValSerPheValSerTrpLysGlyGlu 527
Db 1528 -----GATTCTCTCTTTTGGATAAAGACAATGAGAAATTTCTAAGTGTGAGGGGACC 1581

Qy 528 LysSer----- 529
Db 1582 ACTCACTTACTCGTACACGATGTGCCCTCGAAGATGCTGGCTATTACCGCTGTGCTCGT 1641

Qy 530 -----LysHisSerGlySerLysPhe-----TrpLysAlaLeuArgLeuAlaLeu--- 544
Db 1642 ACATTTGCCATGAAGGCCAGCAATACAACTACTAGGAGTATTGAGCTACGCATCAAG 1701

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; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282,162
; CURRENT FILING DATE: 2002-10-28
; PRIOR FILING DATE: 09/787,835
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 41
; LENGTH: 2709
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-282-162-41

Alignment Scores:
Pred. No.: 1,1e-190 Length: 2709
Score: 1935.00 Matches: 358
Percent Similarity: 99.72% Conservative: 0
Best Local Similarity: 99.72% Mismatches: 1
Query Match: 52.74% Indels: 0
DB: 3 Gaps: 0

US-10-061-727-2 (1-687) x US-10-282-162-41 (1-2709)

QY 1 MetThrLeuLeuTrpCysValValSerLeuTyrPheTyrGlyIleLeuGlnSerAspAla 20
DB 1 ATGGTGCTTCTGTGTGTAGTACTCTACTTTTATGGAATCCTGCAAGTGTATGCC 60

QY 21 SerGluArgCysAspAspTrpGlyLeuAspThrMetArgGlnIleGlnValPheGluAsp 40
DB 61 TCAGAACGCTGGGAGTCTGGGAGCTAGACCATGAGGCAATCCAAAGTGTTCGAAGAT 120

QY 41 GluProAlaArgIleLysCysProLeuPheGluHisPheLeuLysPheAsnTyrSerThr 60
DB 121 GAGCAGCTCGCATCAAGTGGCCACTCTTGAACACTCTTGAATTCACACTACAGCACA 180

QY 61 AlaHisSerAlaGlyLeuThrLeuIleTrpTyrTrpThrArgGlnAspArgAspLeuGlu 80
DB 181 GCCCATTCAGCTGGCTTACTCTGATCTGTTATGAGTCTAGCAGGACCGGACCTTGAG 240

QY 81 GluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTrp 100
DB 241 GAGCCAAATTAATCTCCGCTCCCGAGAACCGCATAGTAAGAGAAAGATGTGCTGTGG 300

QY 101 PheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThr 120
DB 301 TTCCGGCCCACTCTCTCAATGACACTGGCAACTATACCTGATGTTAAGGNACACTACA 360

QY 121 TyrCysSerLysValAlaPheProLeuGluValValGlnLysAspSerCysPheAsnSer 140
DB 361 TATTGAGCAAAAGTGTCAATTTCCCTTGGAAAGTGTTCAAAAAGACAGCTGTTTCAATTC 420

QY 141 ProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArgIleThrCys 160
DB 421 CCCATGAACCTCCAGTGCATAACTGTATATAGAAATATGGCAATTCAGAGGATCACTGT 480

QY 161 ProAsnValAspGlyTyrPheProSerValLysProThrIleThrTrpTyrMetGly 180
DB 481 CCAATGTAGATGGATATTTCTTCCAGTGTCAACCCGACTATCACTTGGTATATGGGC 540

QY 181 CysTyrLysIleGlnAsnPheAsnValIleProGluGlyMetAsnLeuSerPheLeu 200
DB 541 TGTATATAAATACAGAAATTTTAAATATGTAATACCCGAGAGGTATGAACTTGAGTTCTCT 600

QY 201 IleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValThrTyrProGluAsnGly 220
DB 601 ATTGCTCTAAATTTCAAAATTAATGGAATTTACACATGTGTGTGTATATCCAGAAATGGA 660

QY 221 ArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProLysAsnAla 240
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DB 661 CGTACGTTTCATCTCACCAGGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAAATGCA 720

QY 241 ValProProValIleHisSerProAsnAspHisValValTyrGluLysGluProGlyGlu 260
DB 721 GTGCCCTCTGTGATCCATTACCTAATGATCATGTGGTCTATGAGAAAGAACCCAGGAGAG 780

QY 261 GluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAspSerArgAsnGluVal 280
DB 781 GAGTACTCATCTCCCTGTACGGTCTATTTTATGTTTCTGATGGATTCTCGCAATGAGGTT 840

QY 281 TrpTrpThrIleAspGlyLysPheProAspPheThrIleAspValThrIleAsnGlu 300
DB 841 TGGTGGACCAATTGATGGAAAAAACCTGATGACATCACTATTGATGTCCCATTAACGAA 900

QY 301 SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLysLys 320
DB 901 AGTATAAGTCTATAGTAGAACAGAGATGAAACAAGAACTCAGATTTTTCAGCATCAAGAAA 960

QY 321 ValThrSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAlaLysGlyGlu 340
DB 961 GTTACCTCTGAGGATCTCAAGCGAGCTATGTCTGTCATGTAGAGTGCCTCAAGCGGAA 1020

QY 341 ValAlaLysAlaAlaLysValLysGlnLysValProAlaProArgTyrThrValGlu 359
DB 1021 GTTGCCAAAGCAGCCAAAGGTGAAGCAGAAAGTGCCAGCTCCCAAGATACACAGTGCAA 1077

RESULT 10
US-10-282-162-43
; Sequence 43, Application US/10282162
; Patent No. 6927044
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282,162
; CURRENT FILING DATE: 2002-10-28
; PRIOR FILING DATE: 09/787,835
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 43
; LENGTH: 2709
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-282-162-43

Alignment Scores:
Pred. No.: 1,1e-190 Length: 2709
Score: 1935.00 Matches: 358
Percent Similarity: 99.72% Conservative: 0
Best Local Similarity: 99.72% Mismatches: 1
Query Match: 52.74% Indels: 0
DB: 3 Gaps: 0

US-10-061-727-2 (1-687) x US-10-282-162-43 (1-2709)

QY 1 MetThrLeuLeuTrpCysValValSerLeuTyrPheTyrGlyIleLeuGlnSerAspAla 20
DB 1 ATGGTGCTTCTGTGTGTAGTACTCTACTTTTATGGAATCCTGCAAGTGTATGCC 60

QY 21 SerGluArgCysAspAspTrpGlyLeuAspThrMetArgGlnIleGlnValPheGluAsp 40
DB 61 TCAGAACGCTCGGATGACTGGGAGCTAGACCATGAGGCAATCCAAAGTGTTCGAAGAT 120

QY 41 GluProAlaArgIleLysCysProLeuPheGluHisPheLeuLysPheAsnTyrSerThr 60
DB 121 GAGCAGCTCGCATCAAGTGGCCACTCTTGAACACTCTTGAATTCACACTACAGCACA 180

QY 61 AlaHisSerAlaGlyLeuThrLeuIleTrpTyrTrpThrArgGlnAspArgAspLeuGlu 80
DB 181 GCCCATTCAGCTGGCTTACTCTGATCTGTTATGAGTCTAGCAGGACCGGACCTTGAG 240

QY 81 GluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTrp 100
DB 241 GAGCCAAATTAATCTCCGCTCCCGAGAACCGCATAGTAAGAGAAAGATGTGCTGTGG 300

QY 101 PheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThr 120
DB 301 TTCCGGCCCACTCTCTCAATGACACTGGCAACTATACCTGATGTTAAGGNACACTACA 360

QY 121 TyrCysSerLysValAlaPheProLeuGluValValGlnLysAspSerCysPheAsnSer 140
DB 361 TATTGAGCAAAAGTGTCAATTTCCCTTGGAAAGTGTTCAAAAAGACAGCTGTTTCAATTC 420

QY 141 ProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArgIleThrCys 160
DB 421 CCCATGAACCTCCAGTGCATAACTGTATATAGAAATATGGCAATTCAGAGGATCACTGT 480

QY 161 ProAsnValAspGlyTyrPheProSerValLysProThrIleThrTrpTyrMetGly 180
DB 481 CCAATGTAGATGGATATTTCTTCCAGTGTCAACCCGACTATCACTTGGTATATGGGC 540

QY 181 CysTyrLysIleGlnAsnPheAsnValIleProGluGlyMetAsnLeuSerPheLeu 200
DB 541 TGTATATAAATACAGAAATTTTAAATATGTAATACCCGAGAGGTATGAACTTGAGTTCTCT 600

QY 201 IleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValThrTyrProGluAsnGly 220
DB 601 ATTGCTCTAAATTTCAAAATTAATGGAATTTACACATGTGTGTGTATATCCAGAAATGGA 660

QY 221 ArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProLysAsnAla 240
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Db 181 GCCATTGAGTGGCTTACTCTGATCTGGTATTGGACTAGGCAGGACCGGACCTTGAG 240
Qy 81 GluProIleAanPheArgLeuProGluAanArgIleSerLysGluLysAspValLeuTrp 100
Db 241 GAGCAATTAATCTCCGCTCCCGAGAACCGCATTTAGTAAGGAGAAAGATGTCTGTGG 300
Qy 101 PheArgProThrLeuLeuAanAspThrGlyAanTyrThrCysMetLeuArgAanThrThr 120
Db 301 TTCGGGGCCACTCTCCTCAATGACACTGGCAACTATATACCTGTCATGTTAAGGAACACTACA 360
Qy 121 TyrCysSerLysValAlaPheProLeuGluValValGlnLysAspSerCysPheAanSer 140
Db 361 TATTGCGACCAAGTTGATTTCCCTTGGAGTTGTTCAAAAAGACACTGTTTCAATTC 420
Qy 141 ProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArgIleThrCys 160
Db 421 CCCATGAAACTCCCGAGTGCATAAATCTGTATATAGAATATGCAATTCAGAGATCATTGT 480
Qy 161 ProAanValAspGlyTyrPheProSerSerValLysProThrIleThrTrpTyrMetGly 180
Db 481 CCAAAATGTAGATGATATTTTCCCTTCCAGTGTCAAAACCGACTATCACTTGGTATATGGGC 540
Qy 181 CysTyrLysIleGlnAanPheAanValIleProGluGlyMetAanLeuSerPheLeu 200
Db 541 TGTATATAAATACAGAAATTTAATAATGTAATACCCGAAGGTATGAACCTTGAGTTCCCTC 600
Qy 201 IleAlaLeuIleSerAanAanGlyAanTyrThrCysValValThrTyrProGluAanGly 220
Db 601 ATTCGCTTAATTTCAAAATAATGGAATTTACACATGTGTGTGTACATATCCAGAAAATGGA 660
Qy 221 ArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProLysAanAla 240
Db 661 CGTACAGTTTCACTCCACGAGACTCTGACTGTAAGGTAGTAGGCTCTCCAAAAAATGCA 720
Qy 241 ValProValIleHisSerProAanAspHisValValTyrGluLysGluProGlyGlu 260
Db 721 GTGCCCCCTGTGATCCATTTACCTAATGATCATGTGTGTATGAGAAAGAACCGAGAG 780
Qy 261 GluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAanSerArgAanGluVal 280
Db 781 GAGCTACTCATTCCTCTGACGGTCTATTTTAGTTTTTCTGATGGATTCTGCAATGAGTT 840
Qy 281 TrpTrpThrIleAspGlyLysLysProAspAspIleThrIleAspValThrIleAanGlu 300
Db 841 TGGTGGACCAATGATGAAAAAACCCTGATGACATCACTATTGATGTACCATTAACGAA 900
Qy 301 SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLysLys 320
Db 901 AGTATAAGTCTATAGTAAACAGAAAGATGAACCAAGAACTCAGATTTTGAGCATCAAGAA 960
Qy 321 ValThrSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAlaLysGlyGlu 340
Db 961 GTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTCATGCTAGAGTGCCTCAAGCGGAA 1020
Qy 341 ValAlaLysAlaLysValLysGlnLysValProAlaProArgTyrThrValGlu 359
Db 1021 GTTGCCAAAGCAGCAAGGTGAAGGAGAGAAAGTCCAGCTCCAAGATACACAGTGGAA 1077
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RESULT 11

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US-09-313-942-27
; Sequence 27, Application US/09313942
; Patent No. 6472179
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; TITLE OF INVENTION: AND USING
; FILE REFERENCE: REG 203-A
; CURRENT APPLICATION NUMBER: US/09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR FILING DATE: 1999-05-19
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
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; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 2733
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2730)
US-09-313-942-27

Alignment Scores:
Pred. No.: 3,69e-190 Length: 2733
Score: 1930.00 Matches: 357
Percent Similarity: 99.72% Conservative: 0
Best Local Similarity: 99.72% Mismatches: 1
Query Match: 52.60% Indels: 0
DB: 3 Gaps: 0
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US-10-061-727-2 (1-687) x US-09-313-942-27 (1-2733)

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Qy 1 MetThrLeuLeuTrpCysValValSerLeuTyrPheTyrGlyIleLeuGlnSerAspAla 20
Db 1 ATGGTCTTCTGTGGTGTGTAGTGAGTCTCTACTTTTATGGAATCCTGCAAGTGTATGCC 60
Qy 21 SerGluArgCysAspAspTrpGlyLeuAspThrMetArgGlnIleGlnValPheGluAsp 40
Db 61 TCAGAACGCTCGCATGACTGGGACTAGACACCATGAGGCAAAATCCAAGTGTGAAGAT 120
Qy 41 GluProAlaArgIleLysCysProLeuPheGluHisPheLeuLysPheAanTyrSerThr 60
Db 121 GAGCCAGCTCGCATCAAGTCCCACTCTTTGAACACTCTCTTGAATTTCAACTACAGACA 180
Qy 61 AlaHisSerAlaGlyLeuThrLeuIleTyrTrpThrArgGlnAspArgAspLeuGlu 80
Db 181 GCCATTGAGTGGCTTACTCTGATCTGGTATTGGACTAGGCGAGCCGGACCTTGAG 240
Qy 81 GluProIleAanPheArgLeuProGluAanArgIleSerLysGluLysAspValLeuTrp 100
Db 241 GAGCAATTAATCTCCGCTCCCGAGAACCGCATTTAGTAAGGAGAAAGATGTCTGTGG 300
Qy 101 PheArgProThrLeuLeuAanAspThrGlyAanTyrThrCysMetLeuArgAanThrThr 120
Db 301 TTCGGGCCCACTCTCCTCAATGACACTGGCAACTATACCTGTCATGTTAAGGAACACTACA 360
Qy 121 TyrCysSerLysValAlaPheProLeuGluValValGlnLysAspSerCysPheAanSer 140
Db 361 TATTGAGCAAAAGTTGCAATTTCCCTTGGAAAGTTGTTCAAAAAGACAGCTGTTTCAATTC 420
Qy 141 ProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArgIleThrCys 160
Db 421 CCCATGAAACTCCCGAGTGCATAAATCTGTATATAGAATATGCAATTCAGAGATCATTGT 480
Qy 161 ProAanValAspGlyTyrPheProSerSerValLysProThrIleThrTrpTyrMetGly 180
Db 481 CCAAAATGTAGATGGAATATTTCTTCCAGTGTCAAAACCGACTATCACTTGGTATATGGGC 540
Qy 181 CysTyrLysIleGlnAanPheAanValIleProGluGlyMetAanLeuSerPheLeu 200
Db 541 TGTATATAAATACAGAAATTTAATAATGTAATACCCGAAGGTATGAACCTTGAGTTCCCTC 600
Qy 201 IleAlaLeuIleSerAanAanGlyAanTyrThrCysValValThrTyrProGluAanGly 220
Db 601 ATTCGCTTAATTTCAAAATAATGGAATTTACACATGTGTGTGTACATATCCAGAAAATGGA 660
Qy 221 ArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProLysAanAla 240
Db 661 CGTACAGTTTCACTCCACGAGACTCTGACTGTAAGGTAGTAGGCTCTCCAAAAAATGCA 720
Qy 241 ValProValIleHisSerProAanAspHisValValTyrGluLysGluProGlyGlu 260
Db 721 GTGCCCCCTGTGATCCATTTACCTAATGATCATGTGTGTATGAGAAAGAACCGAGAG 780
```

Qy 261 GluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAspSerArgAsnGluVal 280
Db 781 GAGTACTCATTCCCTGTCAGCGTCTATTTTCTGATGGATTCGCAATGAGGT 840
Qy 281 TrpTrpThrIleAspGlyLysProAspIleThrIleAspValThrIleAsnGlu 300
Db 841 TGGTGGACCATTTGATGGAAAAAACCTGATGACATCACTATTGATGTCAACATTAACGAA 900
Qy 301 SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLys 320
Db 901 AGTATAAGTCATAGTAGAACAGAAAGATCAAGAACTCAGATTTTGAGCATCAAGAAA 960
Qy 321 ValThrSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAlaLysGlyGlu 340
Db 961 GTTACTCTGAGGATCTCAGCGCAGCTATGCTGTCATGTAGTAAGTGCACAAAGCGGAA 1020
Qy 341 ValAlaLysAlaLysValLysGlnLysValProAlaProArgTyrThrVal 358
Db 1021 GTTGCCAAAGCAGCCCAAGGTGAAGCAGAAAGTGCCAGCTCCCAAGATACACAGTG 1074

RESULT 12

US-10-282-162-27
; Sequence 27, Application US/10282162
; Patent No. 6927044
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; TITLE OF INVENTION: AND USING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282,162
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 2733
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2730)
US-10-282-162-27

Alignment Scores:

Pred. No.: 3,69e-190 Length: 2733
Score: 1930.00 Matches: 357
Percent Similarity: 99.72% Conservative: 0
Best Local Similarity: 99.72% Mismatches: 1
Query Match: 52.60% Indels: 0
DB: 3 Gaps: 0

US-10-061-727-2 (1-687) x US-10-282-162-27 (1-2733)

Qy 1 MetThrLeuLeuTrpCysValValSerLeuTyrPheTyrGlyIleLeuGlnSerAspAla 20
Db 1 ATGGTGCTTCTGTGGTGTGTAGTGAGTCTCTACTTTTATGGAATCTCTGCAAGTGTGCGC 60
Qy 21 SerGluArgCysAspAspTrpGlyLeuAspThrMetArgGlnIleGlnValPheGluAsp 40
Db 61 TCAGAACCTCGATGACTGGGACTAGACACCATGAGGCAATCCCAAGTGTGTAAGAT 120
Qy 41 GluProAlaArgIleLysCysProLeuPheGluHisPheLeuLysPheAsnTyrSerThr 60
Db 121 GAGCCAGCTCGCATCAAGTGGCCACTCTTTGAACACTTCTTGAATTCACACTACAGACA 180
Qy 61 AlaHisSerAlaGlyLeuThrIleuIleTrpTyrThrArgGlnAspArgAspLeuGlu 80
Db 181 GCCCATTCAGCTGGCCTTACTCTGATCTGTTGATTTGGACTAGGACCGGACCGGACCTTGAG 240

Qy 81 GluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTrp 100
Db 241 GAGCCATTAACCTTCCGCTCCCGAGAACCGCATTTAGTAAGGAGAAAGATGTCTGTGG 300
Qy 101 PheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThr 120
Db 301 TTCGGGCCCATCTCTCTCAATGACACTGGCAACTATACCTGCTGCTGTTAAGGAACACTACA 360
Qy 121 TyrCysSerLysValAlaPheProLeuGluValValGlnLysAspSerCysPheAsnSer 140
Db 361 TATTGCAGCAAAAGTTGCATTTCCCTTGAAGTGTTCCTCAAAAGACAGCTGTTTCAATTCC 420
Qy 141 ProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArgIleThrCys 160
Db 421 CCCATGAACCTCCAGTGCATAACTCTATATAGAATATGCAATTCAGAGATCACTTGT 480
Qy 161 ProAsnValAspGlyTyrPheProSerSerValLysProThrIleThrTyrTyrMetGly 180
Db 481 CCAATGTAGATGATATTTTCTTCCAGTGTCAACCGCACTATCACTTGGTATATGGGC 540
Qy 181 CysTyrLysIleGlnAsnPheAsnAsnValIleProGluGlyMetAsnLeuSerPheLeu 200
Db 541 TGTATAAAATACAGAAATTTTAATAATGTAATACCCGAAGGTATGAACCTTGAGTTTCTC 600
Qy 201 IleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValThrTyrProGluAsnGly 220
Db 601 ATTGCCTTAATTTCAATATATGGAATTTACACATGTGTGTTACATATCCAGAAAAATGA 660
Qy 221 ArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProLysAsnAla 240
Db 661 CGTACGTTTCATCTCACCAGGACTCTGACTGTAAGGTAGTAGGCTCTCCAAAAATGCA 720
Qy 241 ValProProValIleHisSerProAsnAspHisValValTyrGluLysGluProGlyGlu 260
Db 721 GTGCCCCCTGTGATCCATTACCTTAATGATCATGTGTCTATGAGAAAGAACCCAGGAGAG 780
Qy 261 GluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAspSerArgAsnGluVal 280
Db 781 GAGCTACTCATCTCCCTGTCAGGCTCTATTTTAGTTTCTGATGGATTCTCGCAATGAGGT 840
Qy 281 TrpTrpThrIleAspGlyLysLysProAspAspIleThrIleAspValThrIleAsnGlu 300
Db 841 TGGTGGACCATTTGATGGAAAAAACCTGATGACATCACTATTGATGTCAACATTAACGAA 900
Qy 301 SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLys 320
Db 901 AGTATAAGTCATAGTAGAACAGAAAGATGAACAAAGAACTCAGATTTTGGAGCATCAAGAAA 960
Qy 321 ValThrSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAlaLysGlyGlu 340
Db 961 GTTACTCTGAGGATCTCAAGCGCAGCTATGCTGTCATGCTAGTAGTCCCAAGGCGAA 1020
Qy 341 ValAlaLysAlaLysValLysGlnLysValProAlaProArgTyrThrVal 358
Db 1021 GTTGCCAAAGCAGCCCAAGGTGAAGCAGAAAGTGCCAGCTCCCAAGATACACAGTG 1074

RESULT 13

US-10-282-162-33
; Sequence 33, Application US/10282162
; Patent No. 6927044
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; TITLE OF INVENTION: AND USING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282,162
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 33		Db		1837		AGTATAAGTCATAGTAGAAGATGAAACAGAACTCAGATTTTTCAGCATCAAGAAA		1896	
; LENGTH: 2703		Qy		321		ValThrSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAlaLysGlyGlu		340	
; TYPE: DNA		Db		1897		GTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTCTAGTGTCCAAAGGCGAA		1956	
; ORGANISM: Homo sapiens		Qy		341		ValAlaLysAlaLysValLysGlnLysValProAlaProArgTyrThrValGlu		359	
US-10-282-162-33		Db		1957		GTTGCCAAAGCAGCAAGGTGAAGCAGAAAAGTGCCAGCTCCAGATATACAGTGGAA		2013	
Alignment Scores:		RESULT 14							
Pred. No.:	4.62e-180	Length:	2703	US-10-282-162-35		; Sequence 35, Application US/10282162			
Score:	1833.00	Matches:	339			; Patent No. 6927044			
Percent Similarity:	100.00%	Conservative:	0			; GENERAL INFORMATION:			
Best Local Similarity:	100.00%	Mismatches:	0			; APPLICANT: REGENERON PHARMACEUTICALS, INC.			
Query Match:	49.96%	Indels:	0			; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING			
DB:	3	Gaps:	0			; TITLE OF INVENTION: AND USING			
US-10-061-727-2 (1-687) x US-10-282-162-33 (1-2703)						; FILE REFERENCE: REG 203-B-US			
Qy	21	SerGluArgCysAspAspTyrGlyLeuAspThrMetArgGlnIleGlnValPheGluAsp	40			; CURRENT APPLICATION NUMBER: US/10/282,162			
Db	997	TCAGAACGCTCGCATGCTGGGACTAGACACCATGAGGCAATCCAAGTGTTTGAAGAT	1056			; PRIOR FILING DATE: 2002-10-28			
Qy	41	GluProAlaArgIleLysCysProLeuPheGluHisPheLeuLysPheAsnTyrSerThr	60			; PRIOR APPLICATION NUMBER: 09/787,835			
Db	1057	GAGCAGCTCGCATCAAGTGCCTCTCTTGAACACTTCTTGAATTCACACTACAGCACA	1116			; PRIOR FILING DATE: 1999-09-22			
Qy	61	AlaHisSerAlaGlyLeuThrLeuIleTyrThrArgGlnAspArgAspLeuGlu	80			; PRIOR APPLICATION NUMBER: PCT/US99/22045			
Db	1117	GCCCATTCAGCTGGCCCTTACTCTGTATCTGGTATGGACAGGACCGGACCTTGAG	1176			; PRIOR FILING DATE: 1999-09-22			
Qy	81	GluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTyr	100			; NUMBER OF SEQ ID NOS: 56			
Db	1177	GAGCAATTAACCTCCCGCTCCCGAGAACCGCATTAGTAAGGAGAAAGATGTCTGTGG	1236			; SOFTWARE: FastSeq for Windows Version 3.0			
Qy	101	PheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThr	120			; SEQ ID NO 35			
Db	1237	TTCCGGCCCACTCTCTCCATGACACTGGCAACTATACCTGCATGTTAAGGAACTACATA	1296			; LENGTH: 2709			
Qy	121	TyrCysSerLysValAlaPheProLeuGluValGlnLysAspSerCysPheAsnSer	140			; TYPE: DNA			
Db	1297	TATTGAGCAAGTTGCAATTCCTTGGAAAGTTGTTCAAAGACAGCTGTTCATATCC	1356			; ORGANISM: Homo sapiens			
Qy	141	ProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArgIleThrCys	160			US-10-282-162-35			
Db	1357	CCCATGAACTCCCGAGTGCAATAAATCTATATAGATATGCAATTCAGAGCATCACTGT	1416			Alignment Scores:			
Qy	161	ProAsnValAspGlyTyrPheProSerSerValLysProThrIleThrTyrMetGly	180			Pred. No.:		4.64e-180	
Db	1417	CCAAATGTAGATGGATATTTTCCCTCCAGTGTCAAAACCGACTATCACTTGGTATATGGC	1476			Score:		1833.00	
Qy	181	CysTyrLysIleGlnAsnPheAsnValIleProGluGlyMetAsnLeuSerPheLeu	200			Percent Similarity:		100.00%	
Db	1477	TGTTATAAATACAGAAATTTTAAATAGTAATACCCGAAGGTATGAACCTTGAGTTTCCTC	1536			Best Local Similarity:		100.00%	
Qy	201	IleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValThrTyrProGluAsnGly	220			Query Match:		49.96%	
Db	1537	ATTGCTCTTAATTTCAAATAATGAAATTCACATGTGTTGTACATATCCAGAAATGGA	1596			DB:		3	
Qy	221	ArgThrPheHisLeuThrArgThrLeuThrValLysValGlySerProLysAsnAla	240			US-10-061-727-2 (1-687) x US-10-282-162-35 (1-2709)			
Db	1597	CGTACGTTTCATCTCACAGGACTCTGACTGTAAGGTAGTAGGCTCTCCAAAAATGCA	1656			Qy		21	
Qy	241	ValProProValIleHisSerProAsnAspHisValValTyrGluLysGluProGlyGlu	260			Db		997	
Db	1657	GTGCCCTGTGATCCATTCACCTAATGATCATGTGCTCTATGAGAAAGAACAGGAGAG	1716			Qy		41	
Qy	261	GluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAspSerArgAsnGluVal	280			Db		1057	
Db	1717	GAGCTACTCATTCCTGTACGGTCTATTTTAGTTTCTGATGGATTCCTCGCAATGAGGTT	1776			Qy		61	
Qy	281	TyrThrThrIleAspGlyLysLysProAspAspIleThrIleAspValThrIleAsnGlu	300			Db		1057	
Db	1777	TGGTGGACCATTCGATGGAAAAACCTGATGACATCACTATTGATGTCACCATTAACGAA	1836			Qy		61	
Qy	301	SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLysLys	320			Db		1057	

Db 1417 CCAAAATGATAGGATATTTCTTCCAGGTGTCAAACCGCATCATCACTTGGTATATGGGC 1476
Qy 181 CysTyrLysIleGlnAsnPheAsnValIleProGluGlyMetAsnLeuSerPheLeu 200
Db 1477 TGTATAAAATACAGAAATTTTAATAATGTATATACCCGAGGTATGAACCTTGAGTTTCCTC 1536
Qy 201 IleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValThrTyrProGluAsnGly 220
Db 1537 ATTGCTTAATTTCAAAATAATGGAATTTACATGTGTTGTATATATCCAGAAATGGA 1596
Qy 221 ArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProLysAsnAla 240
Db 1597 CGTAGCTTTCATCTCACCGAGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAATAATGCA 1656
Qy 241 ValProProValIleHisSerProAsnAspHisValValTyrGluLysGluProGlyGlu 260
Db 1657 GTGCCCTCTGTATCATCTCACTCAATGATCATGTGGTCTATGAGAAAGAACCCAGGAG 1716
Qy 261 GluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAspSerArgAsnGluVal 280
Db 1717 GAGCTACTCATTCCTGTACGGTCTATTTTAGTTTCTGATGGATTCGCAATGAGGTT 1776
Qy 281 TrpTrpThrIleAspGlyLysLysProAspIleThrIleAspValThrIleAsnGlu 300
Db 1777 TGGTGGACCATTTGATGGAAAAAACCTGATGACATCACTATTGATGTCAACCATTAACGAA 1836
Qy 301 SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLysLys 320
Db 1837 AGTATAAGTCATAGTAGAACAGAAAGTAAACAGAACTCAGATTTTTCAGCATCAAGAAA 1896
Qy 321 ValThrSerGluAspLeuLysArgSerTyrValCysHisAlaAAsqSerAlaLysGlyGlu 340
Db 1897 GTTACCTCTGAGGATCTCAAGCGCAGCTATGCTGTCTATGCTAGAAAGTGCACAGGCGAA 1956
Qy 341 ValAlaLysAlaLysValLysGlnLysValProAlaProArgTyrThrValGlu 359
Db 1957 GTTGCCAAAGCAGCCAGGTGAAGCAGAAAGTGCCAGCTCCCAAGATACACAGTGGAA 2013

RESULT 15

US-10-282-162-37
; Sequence 37, Application US/10282162
; Patent No. 6927044

GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282,162
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PaetSEQ for Windows Version 3.0
; SEQ ID NO 37
; LENGTH: 2709
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-282-162-37

Alignment Scores:
Pred. No.: 4,648-180 Length: 2709
Score: 1833.00 Matches: 339
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 49.96% Indels: 0
Db: 3 Gaps: 0

US-10-061-727-2 (1-687) x US-10-282-162-37 (1-2709)

Qy 21 SerGluArgCysAspAspTrpGlyLeuAspThrMetArgGlnIleGlnValPheGluAsp 40

Db 997 TCAGAACGCTGCGATGACTGGGGACTAGACACCATGAGGCAAAATCCAAGTGTGTTGAAGAT 1056
Qy 41 GluProAlaArgIleLysCysProLeuPheGluHisPheLeuLysPheAsnTyrSerThr 60
Db 1057 GAGCGAGCTCGCATCAAGTGCCCACTCTTTTGAACACTTCTTTGAATTTCAACTACAGCACA 1116
Qy 61 AlaHisSerAlaGlyLeuThrLeuIleTyrTrpThrArgGlnAspArgAspLeuGlu 80
Db 1117 GCCCATTTGAGTGGCTTACTCTGATCTGGTATTGGACTAGCAGGACCGGGACCTTGAG 1176
Qy 81 GluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTrp 100
Db 1177 GAGCAATTAATCTTCCGCTCCCGAGAAACCGCATTTAGTAAGGAGAAAGATGTGCTGTGG 1236
Qy 101 PheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThr 120
Db 1237 TTCCGGGCCCACTCTCCTCAATGACACTGGCAACTATACCTCGCATGTTTAAGGAACACTACA 1296
Qy 121 TyrCysSerLysValAlaPheProLeuGluValValGlnLysAspSerCysPheAsnSer 140
Db 1297 TATTGCGACAAAGTTGCAATTTCCCTTGGAGTTGTTCAAAAAGACAGACTGTTTCANTTCC 1356
Qy 141 ProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArgIleThrCys 160
Db 1357 CCCATGAAACTCCCGAGTGCATAAACTGTATATAGAAATATGSCATTTCAGAGGATCACTTGT 1416
Qy 161 ProAsnValAspGlyTyrPheProSerSerValLysProThrIleThrTyrTrpMetGly 180
Db 1417 CCAAATGTAGATGATATTTTCCCTTCCAGTGTCAAAACCGACTATCACTTGGTATATGGGC 1476
Qy 181 CysTyrLysIleGlnAsnAsnValIleProGluGlyMetAsnLeuSerPheLeu 200
Db 1477 TGTATAAAATACAGAAATTTTAATAATGTATATACCCGAAAGTATGAACTTGAGTTTCCTC 1536
Qy 201 IleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValThrTyrProGluAsnGly 220
Db 1537 ATTGCTTAATTTCAAATAATGGAATTTACACATGTGTTGTATACATATCCAGAAATGGA 1596
Qy 221 ArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProLysAsnAla 240
Db 1597 CGTAGCTTTCATCTCACCGAGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAAAATGCA 1656
Qy 241 ValProProValIleHisSerProAsnAspHisValValTyrGluLysGluProGlyGlu 260
Db 1657 GTGCCCTCTGTATCATCTCACCTAATGATCATGTGCTATGAGAAAGAACCCAGGAGAG 1716
Qy 261 GluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAspSerArgAsnGluVal 280
Db 1717 GAGCTACTCATTCCTGTACGGTCTATTTTAGTTTCTGATGGATTCCTCGCAATGAGGTT 1776
Qy 281 TrpTrpThrIleAspGlyLysLysProAspIleThrIleAspValThrIleAsnGlu 300
Db 1777 TGGTGGACCATTTGATGGAAAAAACCTGATGACATCACTATTGATGTCAACCATTAACGAA 1836
Qy 301 SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLysLys 320
Db 1837 AGTATAAGTCATAGTAGAACAGAAAGTAAACAGAACTCAGATTTTTCAGCATCAAGAAA 1896
Qy 321 ValThrSerGluAspLeuLysArgSerTyrValCysHisAlaAAsqSerAlaLysGlyGlu 340
Db 1897 GTTACCTCTGAGGATCTCAAGCGCAGCTATGCTGTCTATGCTAGAAAGTGCACAGGCGAA 1956
Qy 341 ValAlaLysAlaLysValLysGlnLysValProAlaProArgTyrThrValGlu 359
Db 1957 GTTGCCAAAGCAGCCAGGTGAAGCAGAAAGTGCCAGCTCCCAAGATACACAGTGGAA 2013

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Job time : 359 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 14, 2005, 15:29:38 ; Search time 1402 Seconds
(without alignments)
4052.113 Million cell updates/sec

Title: US-10-061-727-2

Perfect score: 3669

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

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-THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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7: /cgn2_6/ptodata/1/pubna/US10C_PUBCOMB.seq:*
8: /cgn2_6/ptodata/1/pubna/US10D_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubna/US10E_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match Length	ID	Description
1	3667	99.9	2064	US-10-061-727-1
2	3281	89.4	2058	6 US-10-061-727-3
3	2591.5	70.6	4724	5 US-10-167-127-9
4	2591.5	70.6	4724	7 US-10-1717-597-14
5	2580	70.3	1713	5 US-10-215-211-3
6	2327.5	63.4	3355	6 US-10-205-219-24
7	1938	52.8	2748	6 US-10-282-162-51

8	1938	52.8	2748	8	US-10-840-138-21	Sequence 21, Appl
9	1938	52.8	2748	9	US-10-945-068-21	Sequence 21, Appl
10	1938	52.8	2748	10	US-11-056-730-21	Sequence 21, Appl
11	1938	52.8	2748	10	US-11-134-114-51	Sequence 51, Appl
12	1937.5	52.8	2754	6	US-10-282-162-53	Sequence 53, Appl
13	1937.5	52.8	2754	6	US-10-282-162-55	Sequence 55, Appl
14	1937.5	52.8	2754	8	US-10-840-138-23	Sequence 23, Appl
15	1937.5	52.8	2754	8	US-10-840-138-25	Sequence 25, Appl
16	1937.5	52.8	2754	9	US-10-945-068-23	Sequence 23, Appl
17	1937.5	52.8	2754	9	US-10-945-068-25	Sequence 25, Appl
18	1937.5	52.8	2754	10	US-11-056-730-23	Sequence 23, Appl
19	1937.5	52.8	2754	10	US-11-056-730-25	Sequence 25, Appl
20	1937.5	52.8	2754	10	US-11-134-114-53	Sequence 53, Appl
21	1937.5	52.8	2754	10	US-11-134-114-55	Sequence 55, Appl
22	1935	52.7	2703	6	US-10-282-162-39	Sequence 39, Appl
23	1935	52.7	2703	8	US-10-840-138-9	Sequence 9, Appl
24	1935	52.7	2703	9	US-10-945-068-9	Sequence 9, Appl
25	1935	52.7	2703	10	US-11-056-730-9	Sequence 9, Appl
26	1935	52.7	2703	10	US-11-134-114-39	Sequence 39, Appl
27	1935	52.7	2709	6	US-10-282-162-41	Sequence 41, Appl
28	1935	52.7	2709	6	US-10-282-162-43	Sequence 43, Appl
29	1935	52.7	2709	8	US-10-840-138-11	Sequence 11, Appl
30	1935	52.7	2709	8	US-10-840-138-13	Sequence 13, Appl
31	1935	52.7	2709	9	US-10-945-068-11	Sequence 11, Appl
32	1935	52.7	2709	9	US-10-945-068-13	Sequence 13, Appl
33	1935	52.7	2709	10	US-11-056-730-11	Sequence 11, Appl
34	1935	52.7	2709	10	US-11-056-730-13	Sequence 13, Appl
35	1935	52.7	2709	10	US-11-134-114-41	Sequence 41, Appl
36	1935	52.7	2709	10	US-11-134-114-43	Sequence 43, Appl
37	1934	52.7	1077	5	US-10-215-211-5	Sequence 5, Appl
38	1930	52.6	2733	3	US-09-313-942-27	Sequence 27, Appl
39	1930	52.6	2733	3	US-09-935-868-27	Sequence 27, Appl
40	1930	52.6	2733	5	US-10-287-035-27	Sequence 27, Appl
41	1930	52.6	2733	6	US-10-282-162-27	Sequence 27, Appl
42	1930	52.6	2733	8	US-10-840-138-1	Sequence 1, Appl
43	1930	52.6	2733	9	US-10-945-068-1	Sequence 1, Appl
44	1930	52.6	2733	10	US-11-056-730-1	Sequence 1, Appl
45	1930	52.6	2733	10	US-11-134-114-27	Sequence 27, Appl

ALIGNMENTS

RESULT 1
US-10-061-727-1
; Sequence 1, Application US/10061727
; Publication No. US20030170632A1
; GENERAL INFORMATION:
; APPLICANT: Sims, John E.
; APPLICANT: Smith, Dirk E.
; TITLE OF INVENTION: IL-1 RECEPTOR ACCESSORY PROTEIN
; FILE REFERENCE: 3151-A
; CURRENT APPLICATION NUMBER: US/10/061,727
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: US 60/244,831
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 2064
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2064)
; OTHER INFORMATION:
; NAME/KEY: misc feature
; LOCATION: (1792)..(1792)
; OTHER INFORMATION: "n" = a or c. Xaa at amino acid position 598 is Thr or Pro.
US-10-061-727-1

Alignment Scores:
Pred. No.: 0
Score: 3667.00
Length: 2064
Matches: 687

Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 99.95% Indels: 0
 DB: 6 Gaps: 0

US-10-061-727-2 (1-687) x US-10-061-727-1 (1-2064)

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QY 1 MetThrLeuLeuTrpCysValValSerLeuTyrPheTyrGlyIleLeuGlnSerAspAla 20
DB 1 ATGACACTCTCTGGTGTAGTAGTCTCTACTTTTATGGAATCTCTGCAAGTGATGCC 60
QY 21 SerGluArgCysAspAspTrpGlyLeuAspThrMetArgGlnIleGlnValPheGluAsp 40
DB 61 TCAGAACGCTCGCATGACTGGGAGCTAGACACCATGAGGCNAATCCAAAGTGTGAAGAT 120
QY 41 GluProAlaArgIleLysCysProLeuPheGluHisPheLeuLysPheAsnTyrSerThr 60
DB 121 GAGCCAGCTCGCATCAAGTGCCCACTCTTTGAACACATCTTTGAAATTTCAACTACAGACA 180
QY 61 AlaHisSerAlaGlyLeuThrLeuIleTyrTyrTrpThrArgGlnAspArgAspLeuGlu 80
DB 181 GCCAATTCAGTGGCTTACTCTGATCTGGTATTGGACTAGGCGAGGACCGGACCTTGAG 240
QY 81 GluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTyr 100
DB 241 GAGCAATTAACCTCCGCTCCCGAGAACCGCATTAGTAAGAGAAAGATGTCTGTGG 300
QY 101 PheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThr 120
DB 301 TTCGGGCCCACTCTCTCTCAATGACACTGGCAACTATACCTGTCATGTTAAGGAACACTACA 360
QY 121 TyrCysSerLysValAlaPheProLeuGluValValGlnLysAspSerCysPheAsnSer 140
DB 361 TATTGACGCAAGTTGCATTTCCTTGGAAAGTTGTTCAAAAGAACACAGCTGTTTCAATTCC 420
QY 141 ProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArgIleThrCys 160
DB 421 CCCATGAAACTCCAGTGTCATAAATGTATATAGATATGGCATTACAGGATCACTTGT 480
QY 161 ProAsnValAspGlyTyrPheProSerSerValLysProThrIleThrTyrPheMetGly 180
DB 481 CCAAAATGTAGATGATATTTCTCTCCAGTGTCAAACCGACTATCACTTGGTATATGGGC 540
QY 181 CysTyrLysIleGlnAsnPheAsnValIleProGluGlyMetAsnLeuSerPheLeu 200
DB 541 TGTATATAAATACAGAAATTTAATAATGTAATACCCGGAAGGTATGAATTTGAGTTTCCTC 600
QY 201 IleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValThrTyrProGluAsnGly 220
DB 601 ATTGCCCTTAATTTCAATAATGGAAATTACACATGTGTGTTACATATCCAGAAATGGA 660
QY 221 ArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProLysAsnAla 240
DB 661 CGTACGTTTTCTATCCACGAGACTCTGACTGTAAAGTAGTAGGCTCTCCAAAATAATGCA 720
QY 241 ValProProValIleHisSerProAsnAspHisValValTyrGluLysGluProGlyGlu 260
DB 721 GTCCCCCTGTGTATTCACCTAATGATATCATGTGTCTATGAGAAAGAACCCAGAGAG 780
QY 261 GluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAspSerArgAsnGluVal 280
DB 781 GAGCTACTCATTCCTGTACGGTCTATTTTAGTTTTCTGATGATTTCTCGCAATGAGGTT 840
QY 281 TrpTrpThrIleAspGlyLysLysProAspAspIleThrIleAspValThrIleAsnGlu 300
DB 841 TGGTGGACCACTTATGGAAGAAACCTGATGACATCACTATTGATGTCAACATTAAACGAA 900
QY 301 SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLysLys 320
DB 901 AGTATAGTCATAGTAGAAGAGATGAAACAAAGAACTCAGATTTTGTAGCATCAAGAA 960
QY 321 ValThrSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAlaLysGlyGlu 340
DB 1000
  
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DB 1021 GTTGCCAAAGCAGCAAGGTGAAGCAGCAAGTGCAGCTCCAAGATACACAGTGGAACTG 1080
QY 361 AlaCysGlyPheGlyAlaThrValLeuLeuValValIleLeuIleValValTyrHisVal 380
DB 1081 GCTTGTGGTTTTGGAGCCACAGTCCCTAGTGGTGTATCTCATTTGTGTATTACATGTTT 1140
QY 381 TyrTrpLeuGluMetValLeuPheTyrArgAlaHisPheGlyThrAspGluThrIleLeu 400
DB 1141 TACTGGCTAGAGATGTCTCTATTTTACCGGGCTCATTTTGGACAGATGAACCATTTTA 1200
QY 401 AspGlyLysGluTyrAspIleTyrValSerTyrAlaArgAsnAlaGluGluGluPhe 420
DB 1201 GATGGAAGAGATGATGATATTTATGTCATGCAAGGAATGCGGAAGAAAGAATAATTT 1260
QY 421 ValLeuLeuThrLeuArgGlyValLeuGluAsnGluPheGlyTyrLysLeuCysIlePhe 440
DB 1261 GTATTACTGACCTCCGTGGAGTTTTTGGAGAATGAATTTTGGATACAAAGCTGTGCATCTTT 1320
QY 441 AspArgAspSerLeuProGlyGlyAsnThrValGluAlaValPheAspPheIleGlnArg 460
DB 1321 GACCGAGACAGTCTGCTGCTGGGGAAATACAGTGGAGCAGTTTTTGNATTTTCATTCAGA 1380
QY 461 SerArgArgMetIleValValLeuSerProAspTyrValThrGluLysSerIleSerMet 480
DB 1381 AGCAGAAGGATGATGTTGTTCTGAGCCCTGACTATGTGTGACAGAAAGAGCATCAGCATG 1440
QY 481 LeuGluPheLysLeuGlyValMetCysGlnAsnSerIleAlaThrLysLeuIleValVal 500
DB 1441 CTGGAGTTTAAACTGGGTGTCTATGTGCCAGAACTCCATTTGCCACCAAGCTCATTTGGT 1500
QY 501 GluTyrArgProLeuGluHisProHisProGlyIleLeuGlnLysGluSerValSer 520
DB 1501 GAGTACCGTCCCTTGAGCACCCCGCACCCAGGCATTTCTTCAGCTCAAAGAGTCTGTGTCT 1560
QY 521 PheValSerTrpLysGlyGluLysSerLysHisSerGlySerLysPheTrpLysAlaLeu 540
DB 1561 TTTGTGAGCTGGAAAGGAGAAAAAGTCCAAACATTTCTGGCTCTAAATTCGGAAGCTTTG 1620
QY 541 ArgLeuAlaLeuProLeuArgSerLeuSerAlaSerSerGlyTrpAsnGluSerCysSer 560
DB 1621 CGTTTGGCTCTTCCCTGAGAAAGTCTGAGTGCCAGTTCTGGCTGGAAATGAGAGCTGCTCT 1680
QY 561 SerGlnSerAspIleSerLeuAspHisValGlnArgArgSerArgLeuLysGluPro 580
DB 1681 TCCCACTCTGACATCAGTCTGGATCAGTTCAAAGGAGGAGAGTCTGTTTGAAGAGCCC 1740
QY 581 ProGluLeuGlnSerSerGluArgAlaAlaGlySerProProAlaProGly***MetSer 600
DB 1741 CCAGAACTTCAGAGCTCAGAGAGGGCTGCAGGTAGCCCTCCAGCCCCCAGGCNCAATGTCC 1800
QY 601 LysHisArgGlyLysSerSerAlaThrCysArgCysValThrTyrCysGluGlyGlu 620
DB 1801 AAGACCCGAGGGAAGTCTCCCGCCACTCTCCGCTGTGTGTCTACCTACTGTGAAGGAGAG 1860
QY 621 AsnHisLeuArgAsnLysSerArgAlaGluIleHisAsnGlnProGlnTrpGluThrHis 640
DB 1861 AATCACCCTTAGGAACAAGAGCCGGGAGAGATTCATAACAGCCCCCAGTGGGAGACACAC 1920
QY 641 LeuCysLysProValProGlnGluSerGluThrGlnTrpIleGlnAsnGlyThrArgLeu 660
DB 1921 CTCTGTAAAGCTGTTCCCAAGAGTCAGAAACTCAATGGATACAAAATGGCACCAGATTG 1980
QY 661 GluProProAlaProGlnIleSerAlaLeuAlaLeuHisHisPheThrAspLeuSerAsn 680
DB 1981 GAACCCCTTGCTCCCCAGATCTCAGCCCTTGCTCTTCATCATTTTCACGGACTTATCCAAT 2040
QY 681 AsnAsnAspPheTyrIleLeu 687
DB 2041 AACACGACTTTTATATCTCTA 2061
  
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Qy      621 AsnHisLeuArgAsnLysSerArgAlaGluIleHisAsnGlnProGlnTrpGluThrHis 640
Db      1858 AGTCACCTCAGGAGCAGAGCGCGGACAGATGCACACGCATCCCAAGTGGGAAACAC 1917
Qy      641 LeuCysLysProValProGlnGluSerGluThrGlnTrpIleGlnAsnGlyThrArgLeu 660
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Qy      661 GluProProAlaProGlnIleSerAlaLeuAlaLeuHisHisPheThrAspLeuSerAsn 680
Db      1978 GAA---CCCGCTCCCGCAGATCTCAGCTCTTGCACTCCGCCACTTTACAGATTTATCCAAT 2034
Qy      681 AsnAsnAspPheTyrIleLeu 687
Db      2035 AACAAATGACTTTTATATCCTTA 2055

RESULT 3
US-10-167-127-9
; Sequence 9, Application US/10167127
; Publication No. US20030100031A1
; GENERAL INFORMATION:
; APPLICANT: DOWER, STEVEN
; APPLICANT: DUFF, GORDON W.
; TITLE OF INVENTION: INTEGRATIVE ASSAYS FOR MONITORING MOLECULAR ASSEMBLY
; FILE REFERENCE: MSA-026.01 (20974-2601)
; CURRENT APPLICATION NUMBER: US/10/167,127
; PRIOR FILING DATE: 2002-06-11
; PRIOR FILING DATE: 2001-06-11
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 4724
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-167-127-9

Alignment Scores:
Pred. No.: 1,58e-289 Length: 4724
Score: 2591.50 Matches: 502
Percent Similarity: 86.84% Conservative: 39
Best Local Similarity: 80.58% Mismatches: 50
Query Match: 70.63% Indels: 32
DB: 5 Gaps: 7

US-10-061-727-2 (1-687) x US-10-167-127-9 (1-4724)
Qy      1 MetThrLeuLeuTrpCysValSerLeuTyrPheTyrGlyIleLeuGlnSerAspAla 20
Db      207 ATGACACTTCTGTGGTGTGTAGTGTAGTCTCTACTTTTATGGAATCCTGCAAAAGTGTATGCC 266
Qy      21 SerGluArgCysAspAspTrpGlyLeuAspThrMetArgGlnIleGlnValPheGluAsp 40
Db      267 TCNAAACGCTCGCATGACTGGGACTAGACACCATGAGGCAAAATCCAAAGTGTGTAAGAT 326
Qy      41 GluProAlaArgIleLysCysProLeuPheGluHisPheLeuLysPheAsnTyrSerThr 60
Db      327 GAGCCAGCTCGCATCAAGTGGCCCACTCTTTGAACACTTCTTGAATTTCAACTACAGCACA 386
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Qy      61 AlaHisSerAlaGlyLeuThrLeuIleTyrTrpThrArgGlnAspArgAspLeuGlu 80
Db      387 GCCCAATTACGTCGCCCTTACTCTGATCTGGTATTGGACTAGGCAGGACCGGAGACTTGGAG 446
Qy      81 GluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTrp 100
Db      447 GAGCCCAATTAACTTCCGCCCTCCCGAGAACCGCATTAAGTAAGGAGAAAGATGTCTGTGG 506
Qy      101 PheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThr 120
Db      507 TTCGGGCCCACTCTCTCTCAATGACACTGGCACTATACCTGTCATGTTTAAAGAACACATACA 566
Qy      121 TyrCysSerLysValAlaPheProLeuGluValGlnLysAspSerCysPheAsnSer 140
Db      567 TATTGAGCAAAAGTTGCAATTCCCTTGGAAAGTTGTTCAAAAAGACACAGCTGTTTCAATTCC 626
Qy      141 ProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArgIleThrCys 160
Db      627 CCATGAAACTCCCGAGTGCATAAATGATATAGAATATGCGCATTCAGAGGATCAGTTGT 686
Qy      161 ProAsnValAspGlyTyrPheProSerSerValLysProThrIleThrTyrTrpMetGly 180
Db      687 CCAAAATGTAGATGATATTTTCCTTCCAGTGTCAAAACCGACTATCACTTGGTATATGGGC 746
Qy      181 CysTyrLysIleGlnAsnPheAsnAsnValIleProGluGlyMetAsnLeuSerPheLeu 200
Db      747 TGTATATAAAATACAGAAATTTTAATAATGTAATACCCGAGGTATGAATTTGAGTTTCCCTC 806
Qy      201 IleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValThrTyrProGluAsnGly 220
Db      807 ATTGCCCTTAAATTTCAATAATGAAATTTACACATGTGTTGTTTACATATCCAGAAAAATGGA 866
Qy      221 ArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProLysAsnAla 240
Db      867 CGTACGTTTCACTCCACGAGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAAAATGCA 926
Qy      241 ValProProValIleHisSerProAsnAspHisValValTyrGluLysGluProGlyGlu 260
Db      927 GTGCCCCCTGTGATCCATTCCACTAATGATCATGTGCTCTATGAGAAAAAGAACCCAGGAGAG 986
Qy      261 GluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAspSerArgAsnGluVal 280
Db      987 GAGCTACTCATTCCTCGTACGGTCTATTTAGTGTTCCTGATGGATTTCTCGCAATGAGGTT 1046
Qy      281 TrpTrpThrIleAspGlyLysLysProAspAspIleThrIleAspValThrIleAsnGlu 300
Db      1047 TGGTGGACCATTCATGCGNAAAAAAACCTGATGACATCACTATTGATGTCACCATTAAGCAA 1106
Qy      301 SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLysLys 320
Db      1107 AGTATAAGTCAATAGATAGAACAGAAATGAAACAAAGAACTCAGATTTTGGACATCAAGAAA 1166
Qy      321 ValThrSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAlaLysGlyGlu 340
Db      1167 GTTACCTCTGAGGATCTCAAGCGCAGCTATGCTGTGTCATGCTAGAAAGTGCACAAAGCGCAA 1226
Qy      341 ValAlaLysAlaAlaLysValLysGlnLysValProAlaProArgTyrThrValGluLeu 360
Db      1227 GTTGCACCAAGCAGCCCAAGGTGAAGCAGAAAGTGCACAGTCCAGATACACAGTGGAACTG 1286
Qy      361 AlaCysGlyPheGlyAlaThrValLeuLeuValIleLeuIleValValTyrHisVal 380
Db      1287 GCTTGTGGTGTGGAGCCACAGTCTGCTAGTGGTGTATCTCATTGTTGTTTACCATTGTT 1346
Qy      381 TyrTrpLeuGluMetValLeuPheTyrArgAlaHisPheGlyThrAspGluThrIleLeu 400
Db      1347 TACTGGCTAGAGATGCTCTATTTTACCAGGGCTCATTTTGGAAACAGATGAACACATTTTA 1406
Qy      401 AspGlyLysGluTyrAspIleTyrValSerTyrAlaArgAsnAlaGluGluGluPhe 420
Db      1407 GATGAAAGAGATGATGATATTTATGATCTATGCAAGGAATCGCGGAGAGAGAAGAAATTT 1466
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Qy 421 ValLeuLeuThrLeuArgGlyValLeuLeuGluAenGluPheGlyTyTyLysLeuCysIlePhe 440
Db 1467 GTATTACTGACCTCCGTGGAGTTTGGAGATGAATTTGGATACAAAGCTGTGCATCTTT 1526
Qy 441 AspArgAspSerLeuProGlyGlyAsnThrValGluAlaValPheAspPheIleGlnArg 460
Db 1527 GACCAGACAGCTCGCTGGGGGAATTGTACAGATGAGACTTTTGAGCTTCATTTCAGAAA 1586
Qy 461 SerArgArgMetIleValValLeuSerProAspTyTyValThrGluLysSerIleSerMet 480
Db 1587 AGCAGACCCCTCCCTGGTTGTTCTAAGCCCCAACCTACGTGCTCCAGGGAACCAAGCCCTC 1646
Qy 481 LeuGluPheLysLeuGlyValMetCysGlnAenSerIleAlaThrLys----- 496
Db 1647 CTGGAGCTCAAGCTGGCCTA-----GAAATATGGCTCTCGGGGCAACATCAAC 1697
Qy 497 LeuIleValValGluTyArgProLeuGluHisProHisProGlyIleLeuGlnLeuLys 516
Db 1698 GTCATTTTAGTACAGTACAAAGCTGTGAAGGAAACGAAG-----GTGAAGAGAGCTGAAG 1751
Qy 517 GluSer-----ValSerPheValSerTrpLysGlyGluLysSerLysHisSerGly 533
Db 1752 AGGGCTAAGACGGTCTCAGGTCATTAAATGGAAGGGGAAATCCCAAGTATCCACAG 1811
Qy 534 SerLysPheTrpLysAlaLeuArgLeuAlaLeuProLeuArgSerLeuSerAlaSerSer 553
Db 1812 GGCAGTTCTGGAGCAGCTGCAGGTGGCCATGCCAGTGAAGAAAGTCCCGAGCGGTCT 1871
Qy 554 GlyTrpAenGluSerCysSerSerGlnSerAspIleSerLeuAspHisVal-GlnArgAr 573
Db 1872 AGCAGTGATGAGCAGCGGCTCTCGTATTCA-----TCTTTGAAATAATGATGAAGGAA 1925
Qy 573 gArg-----SerArgLeuLysGluProProGluLeuG1 584
Db 1926 TAATGAAAGGTAAGAAAGAACAGAGGGGTCTCCAGGAAGAAAGTCCCGCCAG----- 1980
Qy 584 nSerSerGluArgAlaAlaGlySerProAlaProGly**MetSerLysHisArgG1 604
Db 1981 -----TCTTCATTCGAGTTTATGGTTTCATAGGCAAAAATAATGG 2021
Qy 604 YLysSer 606
Db 2022 TCTAAGC 2028
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RESULT 4

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US-10-717-597-14
; Sequence 14, Application US/10717597
; Publication No. US20040110221A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Burczynski, Michael E.
; APPLICANT: Twine, Natalie C.
; APPLICANT: Dörner, Andrew J.
; APPLICANT: Trepicchio, William L.
; APPLICANT: Slonim, Donna K.
; APPLICANT: Stover, Jennifer A.
; TITLE OF INVENTION: METHODS FOR DIAGNOSING RCC AND OTHER SOLID TUMORS
; FILE REFERENCE: AM101080L
; CURRENT APPLICATION NUMBER: US/10/717,597
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US 60/459,782
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: US 60/427,982
; PRIOR FILING DATE: 2002-11-21
; NUMBER OF SEQ ID NOS: 4904
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 4724
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-717-597-14
Alignment Scores:
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Pred. No.: 1.58e-289 Length: 4724
Score: 2591.50 Matches: 502
Percent Similarity: 86.84% Conservative: 39
Best Local Similarity: 80.58% Mismatches: 50
Query Match: 70.63% Indels: 32
DB: 7 Gaps: 7
US-10-061-727-2 (1-687) x US-10-717-597-14 (1-4724)
Qy 1 MetThrLeuLeuTrpCysValValSerLeuTyTyPheTyTyGlyIleLeuGlnSerAspAla 20
Db 207 ATGACACTTCTGTGTGTGTAGTGTCTACTTTTATGGAATCTCTCAAGATGATGCC 266
Qy 21 SerGluArgCysAspAspTrpGlyLeuAspThrMetArgGlnIleGlnValPheGluAsp 40
Db 267 TCAGAACCTCGATGACTGGGACTAGACACCATGAGGCAATCCAAGTGTTTGGAAGAT 326
Qy 41 GluProAlaArgIleLysCysProLeuPheGluHisPheLeuLysPheAsnTyTySerThr 60
Db 327 GAGCCAGCTCGCATCAAGTGCCTCTTTTGAACACTTCTTTGAAATTCACCTTACAGCACA 386
Qy 61 AlaHisSerAlaGlyLeuThrLeuIleTrpTyTyTrpThrArgGlnAspArgAspLeuGlu 80
Db 387 GCCCATTCAGCTGCCTTACTCTGTATCTGGTATTGGACTAGGCAGGACCGGACCTTGAG 446
Qy 81 GluProIleAenPheArgLeuProGluAenArgIleSerLysGluLysAspValLeuTrp 100
Db 447 GAGCCAAATTAATCTCCGCTCCCGAGAACCGCATTTAGTAAGGAGAAAGATGTGCTGTGG 506
Qy 101 PheArgProThrLeuLeuAsnAspThrGlyAsnTyTyTrpCysMetLeuArgAsnThrThr 120
Db 507 TTCCGGCCCACTCTCTCAATGACACTGGCAACTATACCTGCATGTTTAAGGAACACTACA 566
Qy 121 TyrCysSerLysValAlaPheProLeuGluValValGlnLysAspSerCysPheAsnSer 140
Db 567 TATTGACAGAAAGTTGCAATTTCCCTTGGAAAGTTGTTCAAAAAGACAGCTGTTTCAATTC 626
Qy 141 ProMetLysLeuProValHisLeuLeuTyTyIleGluTyTyGlyIleGlnArgIleThrCys 160
Db 627 CCCATGAACATCCCGAGTGCATAAACTGTATATAGAATATGGCATTCAGAGGATCACTGT 686
Qy 161 ProAsnValAspGlyTyTyPheProSerSerValLysProThrIleThrTrpTyTyMetGly 180
Db 687 CCAATGTAGATGATATTTTCTTCCAGTGTCAACCCGACTATACCTTGGTATATGGGC 746
Qy 181 CysTyTyIleGlnAenPheAsnValIleProGluGlyMetAsnLeuSerPheLeu 200
Db 747 TGTTATAAAATACAGAAATTTTAAATGTAATACCCGGAAGGTATGAACCTTGAGTTTCCTC 806
Qy 201 IleAlaLeuIleSerAsnAenGlyAsnTyTyThrCysValValValThrTyTyProGluAsnGly 220
Db 807 ATTCCTCTTAATTTCAAATAATGGAAATTTACACATGTGTGTGTGTATACATATCCAGAAAATGGA 866
Qy 221 ArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProLysAsnAla 240
Db 867 CGTACGTTTCATCTCACACGAGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAAAATGCA 926
Qy 241 ValProProValIleHisSerProAsnAspHisValValTyTyGluLysGluProGlyGlu 260
Db 927 GTGCCCTCTGTGATCCATTCACCTTAATCATGTGTGTCTATGAGAAAGAACCCAGGAGAG 986
Qy 261 GluLeuLeuIleProCysThrValTyTyPheSerPheLeuMetAspSerArgAsnGluVal 280
Db 987 GAGTACTCATTCCTCTGACGGTCTATTTTAGTTTTCTGTAGGATTCCTCGCAATGAGGTT 1046
Qy 281 TrpTrpThrIleAspGlyLysLysProAspAspIleThrIleAspValThrIleAsnGlu 300
Db 1047 TGGTGGACCATTTGATGGAAAAAACCTGATGACATCACTATTGTATGTCCACCTTAACGAA 1106
Qy 301 SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLysLys 320
Db 1107 AGTATAAGTCATAGTAGAACAAGAGATGAAACAAGAACTCAGATTTTGTAGCATCAAGAAA 1166
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Qy 321 ValThrSerGluAspLeuLysArgSerTyrValCysHisAlaAaSerAlaLysGlyGlu 340
Db 1167 GTTACCTCTGAGGATCTCAAGCGAGTATGTCTCATGTAGAGTGCCAAAGGGCAA 1226
Qy 341 ValAlaLysAlaLysValLysGlnLysValProAlaProArgTyrThrValGluLeu 360
Db 1227 GTTCCAAACAGCCAGGTGAGCAGAAAGTGCAGCTCCAGATACACAGTGGAACTG 1286
Qy 361 AlaCysGlyPheGlyAlaThrValLeuLeuValLileLeuLysValHisVal 380
Db 1287 GCTTGTGGTTTGAGCCACAGTCTCTAGTGTGATCTCTATTGTTGTTTACCATGTT 1346
Qy 381 TyrTrpLeuGluMetValLeuPheTyrArgAlaHisPheGlyThrAspGluThrIleLeu 400
Db 1347 TACTGGCTAGAGATGGTCTATTTTACCGGGCTCATTTTGGAAACAGATGAACCATTTTA 1406
Qy 401 AspGlyLysGluTyrAspIleTyrValSerTyrAlaArgAsnAlaGluGluGluPhe 420
Db 1407 GATGGAAGAAGATGATGATATTTATGTATCTCATCAGGAATGCGGAAGAAGAATTT 1466
Qy 421 ValLeuLeuThrLeuArgGlyValLeuGluAsnGluPheGlyTyrLysLeuCysIlePhe 440
Db 1467 GTATTACTGACCCCTCCGTGGAGTTTGGAGAAATGAAATTTGGATACAAAGCTGTGCATCTT 1526
Qy 441 AspArgAspSerLeuProGlyGlyAsnThrValGluAlaValPheAspPheIleGlnArg 460
Db 1527 GACCGAGACAGTCTGCTCGGGGAATTTGTACAGATGAGACTTTGAGCTTCATTTCAGAAA 1586
Qy 461 SerArgArgMetIleValValLeuSerProAspTyrValThrGluLysSerIleSerMet 480
Db 1587 AGCAGAGCCCTCCTGGTGTCTTAAGGCCCACTACGTCTCCAGGGAACCCAGGCCCTC 1646
Qy 481 LeuGluPheLysLeuGlyValMetCysGlnAsnSerIleAlaThrLys----- 496
Db 1647 CTGGAGCTCAAGGCTGGCCTA-----GAAAAATATGGCTCTCGGGCAACATCAAC 1697
Qy 497 LeuIleValValGluTyrArgProLeuGluHisProHisProGlyIleLeuGlnLys 516
Db 1698 GTCATTTTGTACAGTACAAAGCTGTGAAGGAACGAAG-----GTGAAGAGAGCTGAAG 1751
Qy 517 GluSer-----ValSerPheValSerTrpLysGlyGluLysSerLysHisSerGly 533
Db 1752 AGGCTAAGCGGTGCTCAGCTCATTAATATGGAAGGGAATAATCCAAGTATCCACAG 1811
Qy 534 SerLysPheTrpLysAlaLeuArgLeuAlaLeuProLeuArgSerLeuSerAlaSer 553
Db 1812 GGCAGGTTCTGGAAGCAGCTGCAGTGGCCATGCCAGTGAAGAAAGTCCAGCGGTCT 1871
Qy 554 GlyTrpAsnGluSerCysSerSerGlnSerAspIleSerLeuAspHisVal-GlnArgAr 573
Db 1872 AGCAGTGTATGACGAGCGCCTCTCGTATTCA-----TCTTTGAAAAATGTATGAAGGAA 1925
Qy 573 gATg-----SerArgLeuLysGluProProGluLeuG1 584
Db 1926 TAATGAAAAGGTTAAAGAACACAGGGGTCTCCAGGAAGAAAGAGTCCCCACAG----- 1980
Qy 584 nSerSerGluArgAlaAlaGlySerProProAlaProGly***MetSerLysHisArgG1 604
Db 1981 -----TCTTCATTCGCGAGTTTATGTTTTCATAGGCAAAAAATAATGG 2021
Qy 604 yLysSer 606
Db 2022 TCTAAGC 2028
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RESULT 5

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US-10-215-211-3
; Sequence 3, Application US/10215211
; Publication No. US20030049255A1
; GENERAL INFORMATION:
; APPLICANT: Sims, John E.
; APPLICANT: Smith, Dirk E.
; TITLE OF INVENTION: INTERLEUKIN-1 RECEPTORS IN THE TREATMENT OF DISEASES
; FILE REFERENCE: 3321-A
```

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; CURRENT APPLICATION NUMBER: US/10/215,211
; CURRENT FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: US 60/310,789
; PRIOR FILING DATE: 2001-08-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1713
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1713)
; OTHER INFORMATION:
US-10-215-211-3

Alignment Scores:
Pred. No.: 6,23e-289 Length: 1713
Score: 2580.00 Matches: 487
Percent Similarity: 91.04% Conservative: 31
Best Local Similarity: 85.59% Mismatches: 45
Query Match: 70.32% Indels: 6
DB: 5 Gaps: 3
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US-10-061-727-2 (1-687) x US-10-215-211-3 (1-1713)

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Qy 1 MetThrLeuLeuTrpCysValValSerLeuTyrPheTyrGlyIleLeuGlnSerAspAla 20
Db 1 ATCACACTCTCTGTGGTGTGTAGTGAGTCTCTACTTTTATGGAATCCTGCAAGGTGATGCC 60
Qy 21 SerGluArgCysAspAspTrpGlyLeuAspThrMetArgGlnIleGlnValPheGluAsp 40
Db 61 TCAGAACGCTCGCATGACATGGGGACTAGACACCATGAGGCAAAATCCCAAGTGTTTGAAGAT 120
Qy 41 GluProAlaArgIleLysCysProLeuPheGluHisPheLeuLysPheAsnTyrSerThr 60
Db 121 GAGCCAGCTCGCATCAAGTGCCCACTCTTTGAAACACTCTTTGAAATTCACATCAGCACCA 180
Qy 61 AlaHisSerAlaGlyLeuThrLeuIleTrpTyrTrpThrArgGlnAspArgAspLeuGlu 80
Db 181 GCCCATTCAGCTGGCCTTCTCTGATCTGTGTATTTGACTAGGACGAGCCGGACCTTGAG 240
Qy 81 GluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTrp 100
Db 241 GAGCCCAATTAACCTTCCGCCTCCCGCAGAACCGCATTAGTAAGGAGAAAGATGTCTGTGG 300
Qy 101 PheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThr 120
Db 301 TTCGGCCCCACTCTCTCAATGACACTGGCACTATACCTGCACTGTTTAAAGAACACTACA 360
Qy 121 TyrCysSerLysValAlaPheProLeuGluValValGlnLysAspSerCysPheAsnSer 140
Db 361 TATTGAGCAAAAGTTGCATTTCCCTTGGAAAGTTGTTCAAAAAGACAGACTGTTTCAATTCC 420
Qy 141 ProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArgIleThrCys 160
Db 421 CCCATGAAACTCCAGTGCATAAATGTATATAGAATATATGCAATTCAGAGATCAGTGTGT 480
Qy 161 ProAsnValAspGlyTyrPheProSerSerValLysProThrIleThrTrpTyrMetGly 180
Db 481 CCAATGTAGATGGATATTTTCTTCCAGTGTCAAACCGACTATCATTGTTATATGGGC 540
Qy 181 CysTyrLysIleGlnAsnPheAsnAsnValIleProGluGlyMetAsnLeuSerPheLeu 200
Db 541 TGTATATAAATACAGAAATTTTAATAATACCCGAGGTATGAATTCAGTTCCTCCTC 600
Qy 201 IleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValThrTyrProGluAsnGly 220
Db 601 ATTGCCTTAATTTTCAAAATAATGAAATATACACATGTGTGTTTACATATCCAGAAAAATGGA 660
Qy 221 ArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProLysAsnAla 240
Db 661 CGTACGTTTTCATCTCACAGGACTCTGACTGTGAAGTAGTAGGCTCTCCAAAAAATGCA 720
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Qy 241 ValProValIleHisSerProAsnAepHisValValTyrGluLysGluProGlyGlu 260
Db 721 GTGCCCCCTGTATCCATTCACCTAATGATCATGTGGTCTATGAGAAAGAACCCAGGAG 780
Qy 261 GluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAspSerArgAsnGluVal 280
Db 781 GAGCTACTCATTCCTCGTACGGTCTATTTAGTTTCTGTAGTGATTTCTCGCAATGAGGTT 840
Qy 281 TrpTrpThrIleAspGlyLysValProAspAspIleThrIleAspValThrIleAsnGlu 300
Db 841 TGGTGACCATGTATGAGAAAGAACCTGATGACATCATATTGATGTCCACATTAAACGAA 900
Qy 301 SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLysLys 320
Db 901 AGTATAGTCATAGTACAGAGAGATGAAACAGAACTCAGATTTTGAGCATCAAGAA 960
Qy 321 ValThrSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAlaLysGlyGlu 340
Db 961 GTTACCTCTGAGGATCTCAGCGCAGCTATGCTGTCTATGCTAGAAAGTGCACAAAGCGAA 1020
Qy 341 ValAlaLysAlaAlaLysValLysGlnLysValProAlaProArgTyrThrValGluLeu 360
Db 1021 GTTCCCAAGCAGCAAGGTGACCGCAAAAGTGCAGCTCCACAGATACACAGTGGAACTG 1080
Qy 361 AlaCysGlyPheGlyAlaThrValLeuLeuValValIleLeuIleValValTyrHisVal 380
Db 1081 GCTTGTTGGTTTGGAGCCACAGTCTCTGTAGTGTGATTTCTCATTTGTTTACATGTT 1140
Qy 381 TyrTrpLeuGluMetValLeuPheTyrArgAlaHisPheGlyThrAspGluThrIleLeu 400
Db 1141 TACTGGCTAGAGATGGTCTATTTTACCGGGCTCATTTTGGACAGATGAACCATTTTA 1200
Qy 401 AspGlyLysGluTyrAspIleTyrValSerTyrAlaArgAsnAlaGluGluGluPhe 420
Db 1201 GATGGAAGAAGATGATGATATTTATGTTATCTCTATCAAGGAATGCGGAAGAAGAATTT 1260
Qy 421 ValLeuLeuThrLeuArgGlyValLeuGluAsnGluPheGlyTyrLysLeuCysIlePhe 440
Db 1261 GTTTTACTGACCTCCGTTGGAGTTTGGAGATGAAATTTGGATACAAAGCTGTGATCTTT 1320
Qy 441 AspArgAspSerLeuProGlyGlyAsnThrValGluAlaValPheAspPheIleGlnArg 460
Db 1321 GACCGAGACAGCTCTGCCTGGGGGAATTGTACAGATGAGACTTTTGAGCTTCATTCAGAA 1380
Qy 461 SerArgArgMetIleValValLeuSerProAspTyrValThrGluLysSerIleSerMet 480
Db 1381 AGCAGAGCCCTCTGGTTGTTCTAAGCCCAACTACGTGTCTCAGGGAACCAAGCCCTC 1440
Qy 481 LeuGluPheLysLeuGlyValMetCysGlnAsnSerIleAlaThr--LysLeuIleVal 499
Db 1441 CTGAGCTCAAGCTGGCTAGAAAATATGGGCTCTCGGGCAACATCAACGTCATTTTA 1500
Qy 500 ValGluTyrArgProLeuGluHisProHisProGlyIleLeuGlnLysGluSer-- 518
Db 1501 GTACAGTACAAAGCTGTGAAGAAACGAAG-----GTGAAAGAGCTGAGAGGGCTAAG 1554
Qy 519 -----ValSerPheValSerTrpLysGlyGluLysSerLysHisSerGlySerLysPhe 536
Db 1555 ACGGTGTCTACGGTCATTAATGGAAGGGGAAATCCAAAGTATCCACAGGGCAGGTTT 1614
Qy 537 TrpLysAlaLeuArgLeuAlaLeuProLeuArgSerLeuSerAlaSerSerGlyTrpAsn 556
Db 1615 TGGAAAGCAGCTGCAAGGTGGCCATGCGAGTAAAAAGATGCCAGGGCGTCTAGCAGTGAAT 1674
Qy 557 GluSerCysSerSerGlnSerAspIle 565
Db 1675 GAGCAGGGCCCTCTCGTATTTCATCTTG 1701
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RESULT 6

US-10-205-219-24

; Sequence 24, Application US/10205219

; Publication No. US20030138803A1

; GENERAL INFORMATION:

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; APPLICANT: Warner-Lambert Company
; APPLICANT: Lee, Kevin
; APPLICANT: Dixon, Alistair
; APPLICANT: Brooksbank, Robert
; APPLICANT: Pinnock, Robert
; TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
; FILE REFERENCE: WL-A-018200
; CURRENT APPLICATION NUMBER: US/10/205,219
; CURRENT FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: GB 0118354.0
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 3355
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: Second subunit of the interleukin 1 receptor complex
US-10-205-219-24
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Alignment Scores:

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Pred. No.: 4.97e-259 Length: 3355
Score: 2327.50 Matches: 443
Percent Similarity: 83.36% Conservative: 73
Best Local Similarity: 71.57% Mismatches: 76
Query Match: 63.44% Indels: 28
DB: 6 Gaps: 8
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US-10-061-727-2 (1-687) x US-10-205-219-24 (1-3355)

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Qy 1 MetThrLeuLeuTrpCysValValSerLeuTyrPheTyrGlyIleLeuGlnSerAspAla 20
Db 135 ATGGGACTTCTGTGGTATTTGATGAGTCTGTCTCTTCTATGGGATCCTGCAGAGTCATGCT 194
Qy 21 SerGluArgCysAspAspTrpGlyLeuAspThrMetArgGlnIleGlnValPheGluAsp 40
Db 195 TCGGAGCGCTGTGATGACTCGGGACTAGATACCATCGACAAATCCAAGTGTGTTGAAGAT 254
Qy 41 GluProAlaArgIleLysCysProLeuPheGluHisPheLeuLysPheAsnTyrSerThr 60
Db 255 GAGCGGCTCGAATCAAGTGCCTCTTTGAACACTTCTCTGAAGTACAACTACAGCACT 314
Qy 61 AlaHisSerAlaGlyLeuThrLeuIleTyrTrpThrArgGlnAspArgAspLeuGlu 80
Db 315 GCCATTCCTCTGGCTTACCTCGATCTGGTACTGGACACGAGGAAGACCGGACTGGAG 374
Qy 81 GluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTrp 100
Db 375 GAGCCCATTAACCTCCGCTCCAGAGATCGCATCAGTAAGGAGAAAGATGTCTCTGG 434
Qy 101 PheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThr 120
Db 435 TTCGGGCCCACTCTCTCAATGACACGGGCAATATACACCTGTCATGTTGAGGAACACAACT 494
Qy 121 TyrCysSerLysValAlaPheProLeuGluValValGlnLysAspSerCysPheAsnSer 140
Db 495 TACTGCAGCAAGTTGCAATTCCTTCCCTGGAAGTGTTCAGAAAGGACAGCTGTTCAATTCT 554
Qy 141 ProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArgIleThrCys 160
Db 555 GCCATGAGATTCCTCAGTGCACAGATGTATATTGACATGGCATTTCATAGATCACATGT 614
Qy 161 ProAsnValAspGlyTyrPheProSerSerValLysProThrIleThrTrpTrpMetGly 180
Db 615 CCAAAATGTAGACGATACTTCTCTCCAGTGTCAAACCATCGGTCACTTGTGTATAAGGGT 674
Qy 181 CysTyrLysIleGlnAsnPheAsnAsnValIleProGluGlyMetAsnLeuSerPheLeu 200
Db 675 TGTACTGAAAATAGTGGACTTTCATTAATGTAATACCCGAGGGCATGAACCTTGAGCTTTTC 734
Qy 201 IleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValThrTyrProGluAsnGly 220
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Db 735 ATCCCTTGGTTTCAAAATACGGAATTTACATGTGTGGTTTACATATCTCTGAAACCGGA 794
Qy 221 ArgThrPheHisLeuThrArgThrLeuThrValValGlySerProLysAsnAla 240
Db 795 CGTCTCTTTTCACTTCCACCTCACCAGGACTGTGACTGTAAGGTGGTGGCTCACCNAAGGATGCA 854
Qy 241 ValProProValIleHisSerProAsnAspHisValValTyrGluLysGluProGlyGlu 260
Db 855 TTGCCACCCAGATCTATTCTCCAAATGACCGTGTCTATGAGAAAGAACACGAGGAGAG 914
Qy 261 GluLeuLeuLeuProCysThrValTyrPheSerPheLeuMetAspSerArgAsnGluVal 280
Db 915 GAACCTGGTTATTCCTCCAAAGCTCTATTGAGTTTCAATTATGAGCTCCCAATAGAGTC 974
Qy 281 TrpTrpThrIleAspGlyLysLysProAspAspIleThrIleAspValThrIleAsnGlu 300
Db 975 TGGTGGACCATTTGATGAAAGAGCCTGATGACGTACACGTGCACATCACTATTATATGAA 1034
Qy 301 SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLysLys 320
Db 1035 AGTGTAAATTATTCTTCAACGGAAGATGAAACAGGACTCAGATTTTGGACATCAAGAAA 1094
Qy 321 ValThrSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAlaLysGlyGlu 340
Db 1095 GTCAACCCCGAGGATCTCAGCGCACTATGTCTCATCTCGAATACCAAGGGGAA 1154
Qy 341 ValAlaLysAlaLysValLysGlnLysValProAlaProArgTyrThrValGluLeu 360
Db 1155 GCTGAGCAGGCTGCCAAGGTGAAACAGAGAAAGTCATACCACCAAGGTACACAGTAGAACTC 1214
Qy 361 AlaCysGlyPheGlyAlaThrValLeuLeuValValIleLeuLeuValValTyrHisVal 380
Db 1215 GCCTGTGGTTTGGAGCCACGGCTTTCTCGTAGTGGTTCTCATTTGTGGTTTACCATTGT 1274
Qy 381 TyrTrpLeuGluMetValLeuPheTyrArgAlaHisPheGlyThrAspGluThrIleLeu 400
Db 1275 TACTGGCTGAGATGGTCTCTTTTACCGAGCTCCTTTTGGAAACAGATGAAACAATCTTT 1334
Qy 401 AspGlyLysGluTyrAspIleTyrValSerTyrAlaArgAsnAlaGluGluGluGluPhe 420
Db 1335 GATGGAAGGAGATGATGATATTTATGTTTCTATGCAAGAAATGTGGAAGAGGAAATTT 1394
Qy 421 ValLeuLeuThrLeuArgGlyValLeuGluAsnGluPheGlyTyrLysLeuCysIlePhe 440
Db 1395 GTCTGCTGACGCTGCGTGAGTGTGGAGAATGAGTTTGGATACAAAGCTGTGCATCTTC 1454
Qy 441 AspArgAspSerLeuProGlyGlyAsnThrValGluAlaValPheAspPheIleGlnArg 460
Db 1455 GACAGAGACAGCCTGCTGGGGAAATGTGCAGATGAGACCCTGAGCTTTCATTTCAGAAA 1514
Qy 461 SerArgArgMetIleValValLeuSerProAspTyrValThrGluLysSerIleSerMet 480
Db 1515 AGCAGACGACTCTCTGGTTGCTTAAAGTCCCACTACGTGCTCCAGGGAAACACAAAGCCCTC 1574
Qy 481 LeuGluPheLysLeuGlyValMetCysGlnAsnSerIleAlaThrLys 496
Db 1575 CTGGAGCTCAAGCTGGCCCTA-----GAAATATATGCTCTCCCGGGGCAACATCAAC 1625
Qy 497 LeuIleValValGluTyrArgProLeuGluHisProHisProGlyIleLeuGlnLeuLys 516
Db 1626 GTCATTTTATGTGCTACAAAGCTGTGAAGGACATGAAG-----GTGAAGAGCTGAAG 1679
Qy 517 GluSer-----ValSerPheValSerTrpLysGlyGluLysSerLysHisSerGly 533
Db 1680 CGGGCTAAGACGGTGTCTACGGTCAATTAATGGAAGAGAGAGAAATCCAAGTATCTCTCAG 1739
Qy 534 SerLysPheTrpLysAlaLeuArgLeuAlaLeuProLeuArgSerLeuSerAlaSer 553
Db 1740 GGCAGGTTCTGGAAGCAGTTGCAAGTGGCCATGCCAGTGAAGAG-----AGTCCC 1790
Qy 554 GlyTrpAsnGluSerCysSerGlnSerAspIleSerLeuAspHisValGlnArgArg 573
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Db 1791 AGTGTGTCT-----AGCAATGACAAGCAGGG-TCTCTCTCTACTCATCCCTGAAAAA 1840
Qy 574 ArgSerArgLeuLysGluProGluLeuGlnSerSerGluArgAlaAlaGlySer--- 592
Db 1841 CGTATGAAA-----GGAGAGAGTGAAGGGGTACAAAGAACAAAGCGGTTCATGG 1888
Qy 593 -----ProProAla-ProGly***MetSerLysHisArgGlyLysSerSer 607
Db 1889 GAGGAAGGGCCCCCTCTTCTTAGGCTGTGGCTTCATAGACAGAAAAAGAGT 1943

RESULT 7
US-10-282-162-51
; Sequence 51, Application US/10282162
; Publication No. US20030143697A1
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; TITLE OF INVENTION: AND USING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282,162
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 51
; LENGTH: 2748
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-282-162-51

Alignment Scores:
Pred. No.: 8,27e-214 Length: 2748
Score: 1938.00 Matches: 432
Percent Similarity: 63.42% Conservative: 50
Best Local Similarity: 56.84% Mismatches: 141
Query Match: 52.82% Indels: 140
DB: 19 Gaps: 19

US-10-061-727-2 (1-687) x US-10-282-162-51 (1-2748)
Qy 1 MetThrLeuLeuTrpCysValValSerLeuTyrPheTyrGlyIleLeuGlnSerAspAla 20
Db 1 ATGGTGCTTCTGTGGTGTGTAGTGAAGTCTCTACTTTTATGGAATCTCTCAAGATGATGCC 60
Qy 21 SerGluArgCysAspAspTrpGlyLeuAspThrMetArgGlnIleGlnValPheGluAsp 40
Db 61 TCAGAACGCTGCGATGACCTGGGAGCTAGACACCATGAGGCAATCCCAAGTGTTTGAAGAT 120
Qy 41 GluProAlaArgIleLysCysProLeuPheGluHisPheLeuLysPheAsnTyrSerThr 60
Db 121 GAGCCAGCTCGCATCAAGTGCACCTCTTTGAACTCTTTGAACTCTTGAATTCACACGACA 180
Qy 61 AlaHisSerAlaGlyLeuThrLeuIleTrpTyrTrpThrArgGlnAspArgAspLeuGlu 80
Db 181 GCCCATTCAGCTGGCCCTTACTCTGATCTGCTATTTGGACTAGGCAGGACCGGACCTTGAG 240
Qy 81 GluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTrp 100
Db 241 GAGCAATTAATCTTCGCTCCCGAGAACCCGATTTAGTGAAGAGAAAGATGTGCTGTGG 300
Qy 101 PheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThr 120
Db 301 TTCCGGCCCACTCTCTCTCAATGACACTGCGCACTATACCTGCTGATGTTAAGGAACACTACA 360
Qy 121 TyrCysSerLysValAlaPheProLeuGluValValGlnLysAspSerCysPheAsnSer 140
Db 361 TATTGAGCAAAAGTTGCATTTCCCTTGGAAAGTTGTTCAAAAAAGACAGCTGTTTCAATTCC 420
Qy 141 ProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArgIleThrCys 160
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Db 421 CCCATGAACCTCCAGTCATAACTGTATATAGAAATATGGCAATTCAGAGGATCACTTGT 480
 Qy 161 ProAsnValAspGlyTyrPheProSerSerValLysProThrIleThrTrpTyrMetGly 180
 Db 481 CCAATGTAGATGGATATTTTCCTTCCAGTGTCAAAACCGCATATCATTGGTATATATGGC 540
 Qy 181 CysTyrLysIleGlnAsnPheAsnValIleProGluGlyMetAsnLeuSerPheLeu 200
 Db 541 TGTATAAAATACAGAAATTTTAAATAATGTAATACCCGAAGGTATGAACCTTGAGTTTCCTC 600
 Qy 201 IleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValThrTyrProGluAsnGly 220
 Db 601 ATTGCTTTAAATTTCAAAATTAAGAAATTTACACATGTGTGTGTACATATCCAGAAATGGA 660
 Qy 221 ArgThrPheHleLeuThrArgThrLeuThrValLysValValGlySerProLysAsnAla 240
 Db 661 CGTAGCTTTCATCTCACAGAGCTCTGACTGTAAAGGTAGTAGGCTCTCCAAAATGCA 720
 Qy 241 ValProProValIleHleSerProAsnAspHisValValTyrGluLysGluProGlyGlu 260
 Db 721 GTGCCCTCTGTGATCAATTCACCTAATGATCATGTGGTCTATGAGAAAGAACCCAGGAGAG 780
 Qy 261 GluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAspSerArgAsnGluVal 280
 Db 781 GAGCTACTCATTCCTCTGACGGTCTATTTTATTTTCTGATGGATTCGCAATGAGGTT 840
 Qy 281 TrpTrpThrIleAspGlyLysLysProAspAspIleThrIleAspValThrIleAsnGlu 300
 Db 841 TGGTGGACATTGATGGAAANAAACCTGATGACATCACTATTTGATGTCCACATTAACGAA 900
 Qy 301 SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLysLys 320
 Db 901 AGTATAAGTCATAGTAGAACAGAGAGTGAACAGAACTCAGATTTTGAGCATCAAGAAA 960
 Qy 321 ValThrSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAlaLysGlyGlu 340
 Db 961 GTTACCTCTGAGGATCTCAAGCGCAGCTATGCTGTCTATGTAGAAAGTGCACAAAGGGCAA 1020
 Qy 341 ValAlaLysAlaAlaLysValLysGlnLysValProAlaProArgTyrThrValGluLeu 360
 Db 1021 GTTGGCAAGCAGCCAGGTGAGCAGAAAGTGCAGCTCCAGATACACAGTGCACACA 1080
 Qy 361 -----AlaCysGlyPhe----- 364
 Db 1081 GGGGTGCCAGAGCTGCGGTTCGTGGGAGGCATTACAAGCGGGAGTTTCAGGCTGGA 1140
 Qy 365 GlyAlaThrValLeuValValIleLeuValValTyrHisValTyrTrpLeuGlu 384
 Db 1141 GGGGAGCCTGTAGCCCTGAGCTGAGTGGCCCCCAGGTG-----CCCTACTGTTGTGG 1188
 Qy 385 MetValLeuPheTyrArgAlaHisPhe----- 393
 Db 1189 GCCTCTGTACGCCCGCATCACTGACATGGCATAAATATGACTCTGTAGAGCGGTC 1248
 Qy 394 ---GlyThrAspGluThrIleLeuAspGlyLysGluTyrAspIleTyrValSerTyrAla 412
 Db 1249 CCAGGAGAAGAAGAGACACCGATGGGCCAGGACGGTGTCTGTGGCTTCTCCAGCC 1308
 Qy 413 ArgAsnAlaGluGluGluPheValLeuLeuThrLeuArgGlyValLeuGluAsnGlu 432
 Db 1309 TTGCAGGAGGACTCTGGCACCTAGCTCTGCACACTAGAAATGTCTTACTGTGACAAA 1368
 Qy 433 PheGlyTyrLysLeuCysIlePheAspAspSerLeuProGlyGlyAsnThrValGlu 452
 Db 1369 ATGTCCATTGAGCTCAGAGTTTITGAG-----AATACA---GAT 1404
 Qy 453 AlaValPheAspPheIleGlnArgSerArgMetIle-----ValVal 467
 Db 1405 GCTTCTCTGCGTTCATCTCATCCGCAAAATTTTAACTTGTCAACCTCTGGGGTATTA 1464
 Qy 468 LeuSerProAspTyrValThrGluLysSerIleSerMetLeuGluPheLysLeuGlyVal 487
 Db 1465 GTATGCCCTGAC-----CTGAGTGAATTC----- 1488

Qy 488 MetCysGlnAsnSerIleAlaThrLysLeuIleValValGluTyrArgProLeuGluHis 507
 Db 1489 -----ACCCGTGACAAAACCTGAGTGAAGATTCAATGGTACAG----- 1527
 Qy 508 ProHisProGlyIleLeuGlnLeuLysGluSerValSerPheValSerTrpLysGlyGlu 527
 Db 1528 -----GATTCTCTCTTTTGGATAAAGACAATAGAGAAATTTCTTAAGTGTGAGGGGACC 1581
 Qy 528 LysSer----- 529
 Db 1582 ACTCATTACTCGTACAGATGTGGCCCTGGAAGATGCTGGCTATTACCGCTGTGTCTGT 1641
 Qy 530 -----LysHisSerGlySerLysPhe-----TrpLysAlaLeuArgLeuAlaLeu--- 544
 Db 1642 ACATTTGCCCATGAGGCCAGCAATACACATCACTAGGAGTATTGAGCTACGATCAAG 1701
 Qy 545 -----ProLeuArgSerLeuSerAlaSer 552
 Db 1702 AAAAAAAGAGAGACCATTTCTGTGATCATTTTCCCTCAAGACCATATCAGCTTCT 1761
 Qy 553 SerGlyTrpAsnGluSerCysSerSerGlnSerAspIleSerLeuAspHisValGlnArg 572
 Db 1762 CTGGGG-----TCAAG-ACTGACAATCCCATGTAAGGTGTTTCTGGG 1802
 Qy 573 ArgArgSerArgLeuLysGluProProGluLeuGlnSerSer-----Glu 587
 Db 1803 AACGGGCACACCTTACCAACCATGCTGTGTGGTGGACGGCCNATGACACCCACATAGAGAG 1862
 Qy 588 ArgAlaAlaGlySerPro-----ProAlaProGly***MetSerLys----- 601
 Db 1863 CGCTACCCGGAGCGCGTACCGAGGGGCCACGCGCAAGAAATATTCAGAAAAATAATGA 1922
 Qy 602 -----HisArgGlyLysSerSerAla 608
 Db 1923 GAACATCATTTGAAGTGCCATTGATTTTGTATCTGTGCACAGAGAGGATTTGCACATGGA 1982
 Qy 609 ThrCysArgCysCysValThrTyrCysGluGlyGluAsnHisLeuArgAsnLysSerArg 628
 Db 1983 TTTTAATGTGTGTCTCATTAATACCTGAGTT-TTCAGACACTACGACACCCAGCTCAAGG 2041
 Qy 629 AlaGluIleHisAsnGlnProGlnTrpGluThrHisLeuCysLysProValProGlnGlu 648
 Db 2042 AAGCCTCTCCAGCTTCTCCGGAGAC-AAAACCTACACATGCCCCACCGTGCACGACCT 2100
 Qy 649 SerGluThrGlnTrpIleGlnAsnGlyThrArg-----LeuGluProProAlaProGln 666
 Db 2101 GAA-----CTCCTGGGGGACCGCTCAGTCTTCTCTTCCCCCCCCAAACCCCAAG 2148
 RESULT 8
 US-10-840-138-21
 ; Sequence 21, Application US/10840138
 ; Publication No. US20040224893A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Li-Hsien
 ; APPLICANT: Lin, Hsin Chieh
 ; APPLICANT: Karow, Margaret
 ; TITLE OF INVENTION: Methods of Using IL-1 Antagonists to Treat Neointimal Hyperplasia
 ; FILE REFERENCE: REG 207A
 ; CURRENT APPLICATION NUMBER: US/10/840,138
 ; CURRENT FILING DATE: 2004-05-06
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 21
 ; LENGTH: 2748
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-840-138-21
 Alignment Scores: 8.27e-214 Length: 2748
 Pred. No.: 1938.00 Matches: 432
 Score: 63.42%
 Percent Similarity: 63.42%

Best Local Similarity: 56.84% Mismatches: 141
 Query Match: 52.82% Indels: 140
 DB: 8 Gaps: 19

US-10-061-727-2 (1-687) x US-10-840-138-21 (1-2748)

Qy 1 MetThrLeuLeuTTPCysValValSerLeuTyrPheTyrGlyIleLeuGlnSerAspAla 20
 |||
 Db 1 ATGTTGCTTCTGTGGTGTAGTAGCTCTACCTTTATGGAATCCCGCAAGTGTATGCC 60

Qy 21 SerGluArgCysAspAspTTPGlyLeuAspThrMetArgGlnIleGlnValPheGluAsp 40
 |||
 Db 61 TCAGAACGCTCGCATGACTGGGACTAGACACCATGAGGCAATCCAGTGTGTAAGAT 120

Qy 41 GluProAlaArgIleLysCysProLeuPheGluHisPheLeuLysPheAsnTyrSerThr 60
 |||
 Db 121 GAGCCAGCTCGCATCAAGTGCCTCTCTTTGAACACTCTTTGAATTCACATACAGACA 180

Qy 61 AlaHisSerAlaGlyLeuThrLeuIleTyrTrpThrArgGlnAspArgAspLeuGlu 80
 |||
 Db 181 GCCCATTCAGCTGGCCCTTACTCTGATCTGGTATTGGACTAGGCGAGGACCTTTGAG 240

Qy 81 GluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTyr 100
 |||
 Db 241 GAGCCAAATTAACCTTCGCTCCCGAGAACCGCATTAAGTAAAGAGAAAGATGCTGTGG 300

Qy 101 PheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThr 120
 |||
 Db 301 TTCGGGCCCACTCTCCCTCAATGACACTGGCAACTATACCTGCGATGTTAAGGAACACTTACA 360

Qy 121 TyrCysSerLysValAlaPheProLeuGluValValGlnLysAspSerCysPheAsnSer 140
 |||
 Db 361 TATTGCAGCAAGTTGGATTCCCTTGGAAAGTTGTTCAAAAAGACAGCTGTTCAATTC 420

Qy 141 ProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArgIleThrCys 160
 |||
 Db 421 CCCATGAACCTCCAGCTGCATAAATCTATAGAAATATGCGATTACAGAGATCACTTGT 480

Qy 161 ProAsnValAspGlyTyrPheProSerValLysProThrIleThrTyrMetGly 180
 |||
 Db 481 CCAAAATAGATGGATATTTCTCTTCCAGTGTCAACCGACTATCACTTGGTATATGGGC 540

Qy 181 CysTyrLysIleGlnAsnPheAsnValIleProGluGlyMetAsnLeuSerPheLeu 200
 |||
 Db 541 TGTATATAATACAGAAATTTAATAATGTAATACCCGAAGTATGAACCTTGAGTTCCCTC 600

Qy 201 IleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValThrTyrProGluAsnGly 220
 |||
 Db 601 ATTGCCCTTAATTTCAAATAATGAAATTTACACATGTGTGTTTACATATCCAGAAATGGA 660

Qy 221 ArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProLysAsnAla 240
 |||
 Db 661 CGTACGTTTTCATCTCACAGAGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAAATGCA 720

Qy 241 ValProProValIleHisSerProAsnAspHisValValTyrGluLysGluProGlyGlu 260
 |||
 Db 721 GTCCCCCTGTGATCAATTCACCTAATGATCATGTGCTGTATGAGAAAGAACCCAGAGAG 780

Qy 261 GluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAspSerArgAsnGluVal 280
 |||
 Db 781 GAGCTACTCATTCCTGTACGGTCTATTTTAGTTTCTGATGATTTCTCGCATGAGTT 840

Qy 281 TrpTrpThrIleAspGlyLysLysProAspAspIleThrIleAspValThrIleAsnGlu 300
 |||
 Db 841 TGGTGGACCAATTGATGAAAAAACCTGATGACATCACTATTGATGTCACCATTAACGAA 900

Qy 301 SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLysLys 320
 |||
 Db 901 AGTATAGTCATAGTAGAAGAGATGAAACAAAGAACTCAGATTTTGGAGCATCAAGAA 960

Qy 321 ValThrSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAlaLysGlyGlu 340
 |||
 Db 961 GTTACCTCTGAGGATCTCAAGCCAGCTATGCTGTCATGCTAGTAGTGCCTCAAGGCGAA 1020

Qy 341 ValAlaLysAlaAlaLysValLysGlnLysValProAlaProArgTyrThrValGluLeu 360
 |||
 Db 1021 GTTCCAAAGCAGCCAAAGTGAAGTGAAGAGTCCAGTCCAGATACACAGTGCACACA 1080

Qy 361 -----AlaCysGlyPhe----- 364
 |||
 Db 1081 GGGGTGCCAAGAGCTGCCGGTTTCGTGGAGGCATTACAAAGCGGGAGTTCAGGCTGGAA 1140

Qy 365 GlyAlaThrValLeuLeuValValIleLeuIleValTyrHisValTyrTrpLeuGlu 384
 |||
 Db 1141 GGGGAGCCTGTAGCCCTGAGGTGCCCCAGGTG-----CCCTACTGGTGTGG 1188

Qy 385 MetValLeuPheTyrArgAlaHisPhe----- 393
 |||
 Db 1189 GCCTCTGTACGCCCGCCGCATCAACCTGCATGCGCATAAAAAATGACTCTGTAGGACGGTC 1248

Qy 394 ---GlyThrAspGluThrIleLeuAspGlyLysGluTyrAspIleTyrValSerTyrAla 412
 |||
 Db 1249 CCAGGAGAAAGAGACACCGATGTGGGCCAGGAGGTGCTCTGTGGCTTCTGCCAGCC 1308

Qy 413 ArgAsnAlaGluGluGluPheValLeuLeuThrLeuArgGlyValLeuGluAsnGlu 432
 |||
 Db 1309 TTGCAGGAGGACTCTGGCACCTAGCTCTGCACCTACTAGAAATGCTTCTTACTGTGACAAA 1368

Qy 433 PheGlyTyrLysLeuCysIlePheAspArgAspSerLeuProGlyGlyAsnThrValGlu 452
 |||
 Db 1369 ATGTCCATTGAGCTCAGAGTTTTTGAG-----AATACA---GAT 1404

Qy 453 AlaValPheAspPheIleGlnArgSerArgArgMetIle-----ValVal 467
 |||
 Db 1405 GCTTTCTCCGCTTCATCTCATACCCGCAAAATTTAACTTGTCAACCTCTGGGGTATTA 1464

Qy 468 LeuSerProAspTyrValThrGluLysSerIleSerMetLeuGluPheLysLeuGlyVal 487
 |||
 Db 1465 GTATGCCCTGAC-----CTGAGTGAATTC----- 1488

Qy 488 MetCysGlnAsnSerIleAlaThrLysLeuIleValValGluTyrArgProLeuGluHis 507
 |||
 Db 1489 -----ACCGTGACAAATCGCTGCAAGATCAATGGTACAAG----- 1527

Qy 508 ProHisProGlyIleLeuGlnLysGluSerValSerPheValSerTrpLysGlyGlu 527
 |||
 Db 1528 -----GATTCTCTCTTTGGATAAAGACAATGAGAAATTTCTAAGTGTGAGGGGACC 1581

Qy 528 LysSer----- 529
 |||
 Db 1582 ACTCACTTACTCGTACACGATGTGGCCCTGGAGAGATGCTGGCTATTACCGCTGTGTCCTG 1641

Qy 530 -----LysHisSerGlySerLysPhe-----TrpLysAlaLeuArgLeuAlaLeu--- 544
 |||
 Db 1642 ACATTTGCCCATGAGGCCAGCAATACACATCACTAGGAGTATTGAGCTACGCATCAAG 1701

Qy 545 -----ProLeuArgSerLeuSerAlaSer 552
 |||
 Db 1702 AAAAAAAGAGAGACCATTCCTGTGATCATTTCCCCCTCAAGACCATATCAGCTTCT 1761

Qy 553 SerGlyTrpAsnGluSerCysSerGlnSerAspIleSerLeuAspHisValGlnArg 572
 |||
 Db 1762 CTGGGG-----TCAAG-ACTGACAATCCCATGTAAAGGTGTTCTTCTGGG 1802

Qy 573 ArgArgSerArgLeuLysGluProProGluLeuGlnSerSer-----Glu 587
 |||
 Db 1803 AACCGGCACACCCCTTAAACCACCATGCTGTGGTGGAGCGGCAATGACACCCACATAGAGAG 1862

Qy 588 ArgAlaAlaGlySerPro-----ProAlaProGly***MetSerLys----- 601
 |||
 Db 1863 CGCTTACCAGGAGGCCCGTGCACGAGGGGCCACCGCAGGAATATTCAGAAAAAATAATGA 1922

Qy 602 -----HisArgGlyLysSerSerAla 608
 |||
 Db 1923 GAACATACATTGAAGTCCCATTTGATCTCTGTACAGAGAGAGATTTGACATGGA 1982

Qy 609 ThrCysArgCysCysValThrTyrCysGluGlyGluAenHisLeuArgAsnLysSerArg 628
Db 1983 TTTTAAATGTGTGTCCATAATACCTCAGTT-TTCAGACACTACGCACACAGTCAAGG 2041
Qy 629 AlaGluIleHisAsnGlnProGlnTrpGluThrHisLeuCysLysProValProGlnGlu 648
Db 2042 AAGCCTCTCCAGTGTTCGAGAGAC-AAAACTCACATGCCACCCACCGTCCAGCACCT 2100
Qy 649 SerGluThrGlnTrpIleGlnAenGlyThrArg-----LeuGluProProAlaProGln 666
Db 2101 GAA-----CTCCTGGGGGACCGTCAGTCTTCCTCTCCCCCAAAACCCCAAG 2148

RESULT 9

US-10-945-068-21
; Sequence 21, Application US/10945068
; Publication No. US20050129685A1
; GENERAL INFORMATION:
; APPLICANT: Jingtai Cao
; APPLICANT: Stanley J. Wiegand
; TITLE OF INVENTION: USE OF IL-1 BLOCKERS TO PREVENT CORNEAL INFLAMMATION
; FILE REFERENCE: REG 208A
; CURRENT APPLICATION NUMBER: US/10/945,068
; PRIOR FILING DATE: 2004-09-20
; PRIOR APPLICATION NUMBER: 60/503,854
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 2748
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-945-068-21

Alignment Scores:

Pred. No.: 8.27e-214 Length: 2748
Score: 1938.00 Matches: 432
Percent Similarity: 63.42% Conservative: 50
Best Local Similarity: 56.84% Mismatches: 141
Query Match: 52.82% Indels: 140
DB: 9 Gaps: 19

US-10-061-727-2. (1-687) x US-10-945-068-21 (1-2748)

Qy 1 MetThrLeuLeuTrpCysValValSerLeuTyrPheTyrGlyIleLeuGlnSerAspAla 20
Db 1 ATGTGCTTCTGTGTGTAGTGTGAGTCTCTACTTTTATGGAATCCTGCCAAGTGATGCC 60
Qy 21 SerGluArgCysAspTrpGlyLeuAspThrMetArgGlnIleGlnValPheGluAsp 40
Db 61 TCAGAACGCTCGATGACTGGGACTAGACACCATGAGGCAATCCAAGTGTTTGAAGAT 120
Qy 41 GluProAlaArgIleLysCysProLeuPheGluHisPheLeuLysPheAsnTyrSerThr 60
Db 121 GAGCAGCTCGCATCAGTGGCCACTCTTTGAACACTTCTTGAATTCACACTACAGACA 180
Qy 61 AlaHisSerAlaGlyLeuThrLeuIleTrpTyrTrpThrArgGlnAspArgAspLeuGlu 80
Db 181 GCCCATTCAGTGGCTTACTCTGATCTGGTATTGGACTAGGCGAGGACCGGACCTTGAG 240
Qy 81 GluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTrp 100
Db 241 GAGCCAATTAACTTCCGCTTCCCGAGAACCGCATTAGTAGGAGAAAGATGTCTGTGG 300
Qy 101 PheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuLeuArgAsnThr 120
Db 301 TTCGGGGCCACTCTCTCAATGACACTGGCACTATACCTGCATGTTAAGGAACACTACA 360
Qy 121 TyrCysSerLysValAlaPheProLeuGluValValGlnLysAspSerCysPheAsnSer 140
Db 361 TATTGGAGCAAGTTGCAATTTCCCTTGGAAAGTTGTTCAAAAAGACAGCTGTTCAATTC 420
Qy 141 ProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArgIleThrCys 160

Db 421 CCCATGAATCCCCAGTGCATAAACTGTATATAGATATGCAATTCAGAGGATCACTTGT 480
Qy 161 ProAsnValAspGlyTyrPheProSerSerValLysProThrIleThrTyrTrpMetGly 180
Db 481 CCAAAATGTAGATGATATTTTCTTCCAGTGTCAAAACCGCATATACATTCGTGTATATGGC 540
Qy 181 CysTyrLysIleGlnAsnPheAsnValIleProGluGlyMetAsnLeuSerPheLeu 200
Db 541 TGTATATAATACAGAATTTAATAAGTATATACCCGAGGTATGAATCTGAGTTTCCTC 600
Qy 201 IleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValThrTyrProGluAsnGly 220
Db 601 ATTGCTTAATTTCAAAATTAATGAAATTAACATGTGTGTGTATACATATCCAGAAATGGA 660
Qy 221 ArgThrPheHisLeuThrArgThrLeuThrValLysValGlySerProLysAsnAla 240
Db 661 CGTACGTTTCATCTCACCGAGACTCTGACTGTAAGGTAGTGGCTCTCCAAAAAATGCA 720
Qy 241 ValProProValIleHisSerProAsnAspHisValValTyrGluLysGluProGlyGlu 260
Db 721 GTGCCCCCTGTGATCCATTACCTTAATGATCATGTGTCTATAGAGAAAGAACAGGAGAG 780
Qy 261 GluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAspSerArgAsnGluVal 280
Db 781 GAGCTACTCATTCCTGTGCTGCTATTTTAGTTTCTGATGGATTCTCGCAATGAGGTT 840
Qy 281 TrpTrpThrIleAspGlyLysLysProAspAspIleThrIleAspValThrIleAsnGlu 300
Db 841 TGGTGGACCATTTGATGAAAAAACCCTGATGACATCACTATTGATGTCCACATTAACGAA 900
Qy 301 SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLysLys 320
Db 901 AGTATAAGTCTATAGTACAGAACAGATGAAACAGAACTCAGATTTTGAGGATCAAGAA 960
Qy 321 ValThrSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAlaLysGlyGlu 340
Db 961 GTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTCATGTAGAGTGCCAAAGGCGAA 1020
Qy 341 ValAlaLysAlaLysValLysGlnLysValProAlaProArgTyrThrValGluLeu 360
Db 1021 GTTCCAAAGCAGCCAAAGGTGAAGCAGAAAGTGCCAGTCCCAAGATACACAGTGCACACA 1080
Qy 361 -----AlaCysGlyPhe----- 364
Db 1081 GGGGCTCCAGAGCTGCCGTTCTGTGGAGGCAATTACAAGCGGAGTTTCAGGCTGCAA 1140
Qy 365 GlyAlaThrValLeuLeuValIleLeuIleValValTyrHisValTyrTrpLeuGlu 384
Db 1141 GGGGAGCTGTGAGCCCTGAGGTGCCCGCCAGGTG-----CCCTACTGTTGTGG 1188
Qy 385 MetValLeuPheTyrArgAlaHisPhe----- 393
Db 1189 GCCTCTGTACGCCCGCCGATCAACCTGACATGGCATAAAAATGACTCTGTAGGACGGTC 1248
Qy 394 ---GlyThrAspGluThrIleLeuAspGlyLysGluTyrAspIleTyrValSerTyrAla 412
Db 1249 CCAGGAGAAAGAGACACCGGATGTGGCCCGAGCGGTCTCTGTGGCTTCTGCCAGCC 1308
Qy 413 ArgAsnAlaGluGluGluPheValLeuLeuThrLeuArgGlyValLeuGluAsnGlu 432
Db 1309 TTGCAGGAGGACTCTGCGACCTACGCTCTGCACCTACTAGATAAATGCTCTTACTGTGACAAA 1368
Qy 433 PheGlyTyrLysLeuCysIlePheAspArgAspSerLeuProGlyGlyAsnThrValGlu 452
Db 1369 ATGTCCATTGAGCTCAGAGTTTGTGAG-----AATACA---GAT 1404
Qy 453 AlaValPheAspPheIleGlnArgSerArgArgMetIle-----ValVal 467
Db 1405 GCTTTCCTGCGGTTCATCTCATACCCGCAAAATTTTAACCTTGTCAACCTCTGGGGTATTA 1464
Qy 468 LeuSerProAspTyrValThrGluLysSerIleSerMetLeuLeuGluPheLysLeuGlyVal 487

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Db 1465 GTATGCCCTGAC-----CTGAGTGAATTC----- 1488
Qy 488 MetCysGlnAenSerIleAlaThrLysLeuIleValGluTyrArgProLeuGluHis 507
Db 1489 -----ACCGGTGACAAACTGACGTGAAGATTCAATGGTACAAG----- 1527
Qy 508 ProHisProGlyIleLeuGlnLeuLysGluSerPheValSerTrpLysGlyGlu 527
Db 1528 -----GATTCTCTTCTTTGGATAAAGACAATAGAGAAATTTCTTAAGTGTGAGGGGGACC 1581
Qy 528 LysSer----- 529
Db 1582 ACTCACTTACTCTGACAGATGTGGCCCTGGAAGATGCTGGCTATTACCGCTGTGTCCTG 1641
Qy 530 -----LysHisSerGlySerLysPhe-----TrpLysAlaLeuArgLeuAlaLeu--- 544
Db 1642 ACATTTGCCATGAAGCCAGCAATACACATCACTAGGAGTATTGAGCTACGCATCAAG 1701
Qy 545 -----ProLeuArgSerLeuSerAlaSer 552
Db 1702 AAAAAAAGAAGAGACCATTCCTGTGATCATTTCCCCCTCAAGACCATATCAGCTTCT 1761
Qy 553 SerGlyTrpAenGluSerCysSerGlnSerAspIleSerLeuAapHisValGlnArg 572
Db 1762 CTGGGG-----TCAAG-ACTGACAAATCCCATGTAAGTGTTCTGGG 1802
Qy 573 ArgArgSerArgLeuLysGluProProGluGlnSerSer-----Glu 587
Db 1803 AACCGGCACACCCCTTACCACCATGCTGTGTGGAGCGGCCAATGACACCCACATAGAGAG 1862
Qy 588 ArgAlaAlaGlySerPro-----ProAlaProGly***MetSerLys----- 601
Db 1863 CGCCTACCGGGAGCGCGGTGACCGAGGGGCCACGCGCAAGATATTCAGAAAAATAATGA 1922
Qy 602 -----HisArgGlyLysSerSerAla 608
Db 1923 GAACATCATTAAGTGCCATTGATTTTGTGATCTGTCACAGAGAGGATTTGCACATGGA 1982
Qy 609 ThrCysArgCysCysValThrTyrCysGluGlyGluAsnHisLeuArgAenLysSerArg 628
Db 1983 TTTTAAATGTGTGTCCATAATACCCCTGAGTT- TTCAGACACATACGCCACACAGTCAAGG 2041
Qy 629 AlaGluIleHisGlnProGlnTrpGluThrHisLeuCysLysProValProGlnGlu 648
Db 2042 AAGCCTCCTCCAGTCTCTCCGGAGAC-AAAACTCACACATGCCACCGTCCCGCCAGCACCT 2100
Qy 649 SerGluThrGlnTrpIleGlnAenGlyThrArg-----LeuGluProProAlaProGln 666
Db 2101 GAA-----CTCCTGGGGGGACCGTCAAGTCTTCTCTTCCCCCAAAACCCAAG 2148
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RESULT 10

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US-11-056-730-21
; Sequence 21, Application US/11056730
; Publication No. US20050197293A1
; GENERAL INFORMATION:
; APPLICANT: Mellis, Scott
; APPLICANT: Stahl, Neil
; APPLICANT: Radin, Allen
; APPLICANT: Weinstein, Steven
; APPLICANT: Calaprice, Denise
; APPLICANT: Karow, Margaret
; APPLICANT: Papadopoulos, Joanne
; TITLE OF INVENTION: Use of an IL-1 Antagonist for Treating Arthritis
; FILE REFERENCE: 203G
; CURRENT APPLICATION NUMBER: US/11/056,730
; CURRENT FILING DATE: 2005-02-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 2748
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
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; OTHER INFORMATION: Synthetic

US-11-056-730-21

Alignment Scores:

Pred. No.:	8,27e-214	Length:	2748
Score:	1938.00	Matches:	432
Percent Similarity:	63.42%	Conservative:	50
Best Local Similarity:	56.84%	Mismatches:	141
Query Match:	52.82%	Indels:	140
DB:	10	Gaps:	19

US-10-061-727-2 (1-687) x US-11-056-730-21 (1-2748)

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Qy 1 MetThrLeuLeuTrpCysValValSerLeuTyrPheTyrGlyIleLeuGlnSerAspAla 20
Db 1 ATGGTCTCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 60
Qy 21 SerGluArgCysAspAspTrpGlyLeuAapThrMetArgGlnIleGlnValPheGluAsp 40
Db 61 TCAGAAACGCTGCGATGACTGGGACCTAGACACCATGAGGCAATCCAAAGTGTTTGAAGAT 120
Qy 41 GluProAlaArgIleLysCysProLeuPheGluHisPheLeuLysPheAenTyrSerThr 60
Db 121 GAGCCAGCTCGCATCAAGTGCCACCTCTTTGAACACTTCTTGAATTCACACTACAGACA 180
Qy 61 AlaHisSerAlaGlyLeuThrLeuIleTrpTyrThrArgGlnAspArgAspLeuGlu 80
Db 181 GCCATTACGTGGCCCTTACTCTGTATCTGTATTGGACTAGGACGACCGGACCTTGAG 240
Qy 81 GluProIleAenPheArgLeuProGluAenArgIleSerLysGluLysAspValLeuTrp 100
Db 241 GAGCCAAATTAACCTTCCGCTCCCGAGAACCGCATTTAGTAAGAGAGAAAGATGTGCTGG 300
Qy 101 PheArgProThrLeuLeuAenAspThrGlyAenTyrThrCysMetLeuArgAenThrThr 120
Db 301 TTCGGGCCCACTCTCTCAATGACACTGGCAACTATACCTGTCATGTTAAGGAACACTACA 360
Qy 121 TyrCysSerLysValAlaPheProLeuGluValValGlnLysAspSerCysPheAenSer 140
Db 361 TATTGAGCAAAAGTTGCAATTTCCCTTTGGAAAGTTGTTCAAAAAGACAGCTGTTTCAATTC 420
Qy 141 ProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArgIleThrCys 160
Db 421 CCATGAAACTCCCATGTCATAAATGTTATATAAGATATGGCAATTCAGAGATCATTGT 480
Qy 161 ProAenValAspGlyTyrPheProSerSerValLysProThrIleThrTrpTyrMetGly 180
Db 481 CCATAATGTAGATGGATATTTCCTTCCAGTGTCAAACCGACTATCACTTGGTATATGGGC 540
Qy 181 CysTyrLysIleGlnAenPheAenValIleProGluGlyMetAenLeuSerPheLeu 200
Db 541 TGTATATAAATAACAGAAATTTTAATAATGTAATACCCGAAAGGTATGAACTTGAGTTTCCTC 600
Qy 201 IleAlaLeuIleSerAenAenGlyAenTyrThrCysValValThrTyrProGluAenGly 220
Db 601 ATTGCCTTAAATTTCAAATAATGGAATATACACATGTGTGTATACATATCCAGAAAAATGGA 660
Qy 221 ArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProLysAenAla 240
Db 661 CGTACGTTTCATCTCACAGGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAAAATGCA 720
Qy 241 ValProProValIleHisSerProAenAspHisValValTyrGluLysGluProGlyGlu 260
Db 721 GTGCCCTCTGTGATCCATTCACCTAATGATCATGTGCTCTATGAGAAAGAACCCAGGAGAG 780
Qy 261 GluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAspSerArgAenGluVal 280
Db 781 GAGCTACTCATTCCTGTCGGTCTATTATTAGTTTCTGATGATTTCTCCCAATGAGGTT 840
Qy 281 TrpTrpThrIleAspGlyLysLysProAspAspIleThrIleAspValThrIleAenGlu 300
Db 841 TGGTGGACCATGATGGAAAAAACCCTGATGACATCACTATTTCATGTCACCATTAACGAA 900
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QY 81 GluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTyr 100
Db 241 GAGCCAAATTAATCTCCGCCCTCCCGAGAACCGCATTTAGTAGGAGAAAGATGTCTGTGG 300
QY 101 PheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThr 120
Db 301 TTCCGGCCCACTCTCCTCAATGACACTGGCACTATATACCTGCATGTTTAAGGAACACTACA 360
QY 121 TyrCysSerLysValAlaPheProLeuGluValValGlnLysAspSerCysPheAsnSer 140
Db 361 TATTGCAGCAAGATTGCATTTCCCTTGGAGTGTCTCAAAAAGACAGCTGTTTCAATTCC 420
QY 141 ProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArgIleThrCys 160
Db 421 CCCATGAACATCCCAAGTGCATAAACTGTATATAGATATATGCAATTCAGAGGATCACATTGT 480
QY 161 ProAsnValAspGlyTyrPheProSerSerValLysProThrIleThrTyrTyrMetGly 180
Db 481 CCAATGTAGATGATATTTTCCCTTCCAGTGTCAACCGACTATCATTTGGTATATGGGC 540
QY 181 CysTyrLysIleGlnAsnPheAsnAsnValIleProGluGlyMetAsnLeuSerPheLeu 200
Db 541 TGTATATAAATACAGAAATTTAATAATGTAATACCCGAAGTATGAACCTTGAGTTTCCCTC 600
QY 201 IleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValThrTyrProGluAsnGly 220
Db 601 ATTGCCCTTAATTTCAAAATAATGGAATTTACACATGTGTGTATCATATCCAGAAAAATGGA 660
QY 221 ArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProLysAsnAla 240
Db 661 CGTACGTTTCATCTCACAGAGACTCTGACTGTAAAGTAGTAGGCTCTCCAAAAAATGCA 720
QY 241 ValProProValIleHisSerProAsnAspHisValValTyrGluLysGluProGlyGlu 260
Db 721 GTGCCCCCTGTATCCATTACCTTAATGATCATGTGTCTATGAGAAAGAACCCAGGAGAG 780
QY 261 GluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAspSerArgAsnGluVal 280
Db 781 GAGCTACTCATTCCTGTACGGTCTATTTAGTTTCTGATGAGTTCCTGCAATGAGGTT 840
QY 281 TrpTrpThrIleAspGlyLysLysProAspAspIleThrIleAspValThrIleAsnGlu 300
Db 841 TGGTGGACCAATTGATGGAAAAAACCCTGATGACATCATCTATTGATGTCACCATTTAAGAA 900
QY 301 SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLysLys 320
Db 901 AGTATAAGTCATAGTAAACAGAGAATGAAACAAAGAACTCAGATTTTGACCATCAAGAA 960
QY 321 ValThrSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAlaLysGlyGlu 340
Db 961 GTTACTCTGAGGATCTCAAGCCGAGCTATGTCTGTCTATGATCTAGAAAGTGCACAAAGCGAA 1020
QY 341 ValAlaLysAlaAlaLysValLysGlnLysValProAlaProArgTyrThrValGluLeu 360
Db 1021 GTTGCCAAAGACGCCAAGGTGAAGCAGAAAGTCCAGCTCCAAGATACACAGTGCACACA 1080
QY 361 -----AlaCysGlyPhe----- 364
Db 1081 GGGGCTGCCAAGAGCTGCCGGTTTCGTGGGAGGCATTACAAGCGGGAGTTTCAGGCTGGAA 1140
QY 365 GlyAlaThrValLeuLeuValValIleLeuIleValValTyrHisValTyrTrpLeuGlu 384
Db 1141 GGGGAGCCTGTAGCCCTGAGGTGCCCCAGGTG-----CCCTACTGGTTGTGG 1188
QY 385 MetValLeuPheTyrArgAlaHisPhe----- 393
Db 1189 GCCTCTGTAGCCCCCGCATCACTGACATGTCATGCAATAAAATGATCTCTGCTAGGACGGTC 1248
QY 394 ---GlyThrAspGluThrIleLeuAspGlyLysGluTyrAspIleTyrValSerTyrAla 412
Db 1249 CCAGGAGAAAGACAGACACGAGTGTGGCCCGACGAGCGGTCTCTGTGCTTCTGCCAGCC 1308

QY 413 ArgAsnAlaGluGluGluGluPheValLeuLeuThrLeuArgGlyValLeuGluAsnGlu 432
Db 1309 TTGCAGGAGGACTCTGGCAGCTAGCTAGCTACTAGATAAAATGCTTCTTACTGTGACAAA 1368
QY 433 PheGlyTyrLysLeuCysIlePheAspArgAspSerLeuProGlyGlyAsnThrValGlu 452
Db 1369 ATGTCCATTGAGCTCAGAGTTTITGAG-----AATACA---GAT 1404
QY 453 AlaValPheAspPheIleGlnArgSerArgArgMetIle-----ValVal 467
Db 1405 GCITTCCTGCGGTTCATCTCATACCCGCAAAATTTAACTTGTCAACCTCTGGGGTATTA 1464
QY 468 LeuSerProAspTyrValThrGluLysSerIleSerMetLeuGluPheLysLeuGlyVal 487
Db 1465 GTATGCCCTGAC-----CTGAGTGAATTC----- 1488
QY 488 MetCysGlnAsnSerIleAlaThrLysLeuIleValValGluTyrArgProLeuGluHis 507
Db 1489 -----ACCGTGACAAAACCTGAGTGAAGATCAATGGTACAAG----- 1527
QY 508 ProHisProGlyIleLeuGlnLeuLysGluSerValSerPheValSerTrpLysGlyGlu 527
Db 1528 -----GATTCTCTCTTTTGGGATAAAGACAATGAGAAATTTCTAAGTGTGAGGGGACC 1581
QY 528 LysSer----- 529
Db 1582 ACTCACTTACTCTACACGATGTGGCCCTGGAAGATGCTGGCTATTACCGCTGTGCTGTG 1641
QY 530 -----LysHisSerGlySerLysPhe-----TrpLysAlaLeuArgLeuAlaLeu--- 544
Db 1642 ACATTTGCCCATGAAGCCGCAATCAACATCACTAGGAGTATTGAGCTACCGCATCAAG 1701
QY 545 -----ProLeuArgSerLeuSerAlaSer 552
Db 1702 AAAAAAAGAGAGACCATTCCTGTGTATCTTCCCTCTCAAGCCATATCAGCTTCT 1761
QY 553 SerGlyTyrAsnGluSerCysSerGlnSerAspIleSerLeuAspHisValGlnArg 572
Db 1762 CTGGGG-----TCAAG-ACCTGACAATCCCATGTAAGGTGTTTCTGGG 1802
QY 573 ArgArgSerArgLeuLysGluProGluLeuGlnSerSer-----Glu 587
Db 1803 AACCCGCACACCTTAAACCACTATGCTGTGTGGAGCGGCAATGACACCCACATAGAGAG 1862
QY 588 ArgAlaAlaGlySerPro-----ProAlaProGly***MetSerLys----- 601
Db 1863 CGCCTACCCGGGAGCGCGGTGACCCGCGGCGCCAGGAGGATATTTCAGAAAATATGA 1922
QY 602 -----HisArgGlyLysSerSerAla 608
Db 1923 GAACTACATTGAAGTGCCATTGATTTTGTATCTGTCAACAGAGAGGATTTGCACATGGA 1982
QY 609 ThrCysArgCysCysValThrTyrCysGluGlyGluAsnHisLeuArgAsnLysSerArg 628
Db 1983 TTTTAAATGTGTGTCCATAATACCTCGAGTT--TTCAGACACTACCGACCCAGCTCAAGG 2041
QY 629 AlaGluIleHisAsnGlnProGlnTrpGluThrHisLeuCysLysProValProGlnGlu 648
Db 2042 AAGCCTCTCCAGTTCTCCGAGAC-AAAACCTCACACATGCCCGCCCGTCCCGACACCT 2100
QY 649 SerGluThrGlnTrpIleGlnAsnGlyThrArg-----LeuGluProProAlaProGln 666
Db 2101 GAA-----CTCCTGGGGGAGCGGTCTCAGTCTCTCTCTCCCGCCCAAAACCAAG 2148

RESULT 12

US-10-282-162-53

; Sequence 53, Application US/10282162

; Publication No. US20030143697A1

; GENERAL INFORMATION:

; APPLICANT: REGENERON PHARMACEUTICALS, INC.

; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING

; TITLE OF INVENTION: AND USING

; FILE REFERENCE: REG 203-B-US

; CURRENT APPLICATION NUMBER: US/10/282,162
 ; CURRENT FILING DATE: 2002-10-28
 ; PRIOR APPLICATION NUMBER: 09/787,835
 ; PRIOR FILING DATE: 1999-09-22
 ; PRIOR APPLICATION NUMBER: PCT/US99/22045
 ; PRIOR FILING DATE: 1999-09-22
 ; NUMBER OF SEQ ID NOS: 56
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 53
 ; LENGTH: 2754
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-282-162-53

Alignment Scores:
 Pred. No.: 9,49e-214 Length: 2754
 Score: 1937.50 Matches: 432
 Percent Similarity: 62.06% Conservative: 49
 Best Local Similarity: 55.74% Mismatches: 135
 Query Match: 52.81% Indels: 161
 DB: 6 Gaps: 20

US-10-061-727-2 (1-687) x US-10-282-162-53 (1-2754)

QY 1 MetThrLeuLeuTrpCysValValSerLeuTyrPheTyrGlyIleLeuGlnSerAspAla 20
 DB 1 ATGGTGCTTCTGTGTGTGTAGTGTCTTCTTCTTATGGNAATCTCGCAAGTGTGCC 60
 QY 21 SerGluArgCysAspAspTrpGlyLeuAspThrMetArgGlnIleGlnValPheGluAsp 40
 DB 61 TCAGAACGCTGCATGACTGGGGACTAGACACCATGAGGCAAAATCCAAGTGTGTGAAGAT 120
 QY 41 GluProAlaArgIleLysCysProLeuPheGluHisPheLeuLysPheAsnTyrSerThr 60
 DB 121 GAGCAGCTCGCATCAAGTGCCACTCTTTGAACACTCTTTGAATTCACACTACAGCACA 180
 QY 61 AlaHisSerAlaGlyLeuThrLeuIleTrpTyrTrpArgGlnAspArgAspLeuGlu 80
 DB 181 GCCCATTCAGCTGGCTTACTCTGATCTGTATTTGGACTAGCAGGACCGGGACCTTGAG 240
 QY 81 GluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTrp 100
 DB 241 GAGCCAAATTAATCTCCGCTCCCGAGAACCGCATTAGTAAGGAGAAAGATGTGTGTGG 300
 QY 101 PheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThr 120
 DB 301 TTCGGCCCACTCTCCTCAATGACACTGGCACTATACCTGCATGTTAAGGAACACTACA 360
 QY 121 TyrCysSerLysValAlaPheProLeuGluValValGlnLysAspSerCysPheAsnSer 140
 DB 361 TATTGCACAAAGTTGCAATTTCCCTTGGAGTTGTTCAAAAAGACAGCTGTTCAATTC 420
 QY 141 ProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArgIleThrCys 160
 DB 421 CCCATGAACCTCCAGTCATAACTGATATAGAAATATGCAATATGCAATTCAGAGATCATTGT 480
 QY 161 ProAsnValAspGlyTyrPheProSerSerValLysProThrIleThrTrpTyrMetGly 180
 DB 481 CCNAATGTAGATGGATATTTTCCCTCCAGTGTCAAAACCGACTATCACTTGTATATGGGC 540
 QY 181 CysTyrLysIleGlnAsnPheAsnValIleProGluGlyMetAsnLeuSerPheLeu 200
 DB 541 TGTATATAAATACAGAAATTTAATATGTAATACCCGAAAGGTATGAACTTGAGTTTCCTC 600
 QY 201 IleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValThrTyrProGluAsnGly 220
 DB 601 ATTGCTTAAATTCAAATAATGGAATTTACACATGTGTGTTTACATATCCAGAAAAATGGA 660
 QY 221 ArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProLysAsnAla 240
 DB 661 CGTAGTTTCTATCTCACCAGGACTCTGACTGTAAGAGGTAGTAGGCTCTCCAAAAAATGCA 720
 QY 241 ValProProValIleHisSerProAsnAspHisValValTyrGluLysGluProGlyGlu 260

DB 721 GTGCCCCCTGTGTATCCATTCACCTAATGATCATGTGGTCTATGAGAAAGAACCCAGGAG 780
 QY 261 GluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAspSerArgAsnGluVal 280
 DB 781 GAGTACTCATTCCTGTACGGTCTATTTTATGTTTCTGTAGTGGATTCGCAANTGAGTT 840
 QY 281 TrpTrpThrIleAspGlyLysLysProAspAspIleThrIleAspValThrIleAsnGlu 300
 DB 841 TGGTGGACCATTTGATGGAAAAAACCTGATGACATCACTATTGATGTCCCATTAACGAA 900
 QY 301 SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLysLys 320
 DB 901 AGTATAAGTCATAGTAGAACAGAGATGAACAAGAACTCAGATTTTGAGCATCAAGAAA 960
 QY 321 ValThrSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAlaLysGlyGlu 340
 DB 961 GTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTATGTAGTAAGTGCACAAAGCGAA 1020
 QY 341 ValAlaLysAlaAlaLysValLysGlnLysValProAlaProArgTyrThrValGluLeu 360
 DB 1021 GTTCCCAAGCAGCAAGGTGAGCAGAAAGTGCAGCTCCAGATACACAGTGCACACA 1080
 QY 361 -----AlaCysGlyPhe----- 364
 DB 1081 GGGGCTGCCAGAACTGCCGGTTTCGTGGGAGGCATTACAAAGCGGAGTTCAGGCTGCAA 1140
 QY 365 GlyAlaThrValLeuLeuValValIleLeuIleValValTyrHisValTyrTrpLeuGlu 384
 DB 1141 GGGGAGCTGTAGCCCTGAGGTGCCCGCCAGGTG-----CCCTACTGTTGTGG 1188
 QY 385 MetValLeuPheTyrArgAlaHisPhe----- 393
 DB 1189 GCCTCTGAGCCCCCGCATCACTGACATGGCATAAATAATGACTCTGTAGGACGGTC 1248
 QY 394 ---GlyThrAspGluThrIleLeuAspGlyLysGluTyrAspIleTyrValSerTyrAla 412
 DB 1249 CCAGGAGAAGAGAGACACGAGTGTGGCCCGCAGGCGGTCTCTGTGGCTTCTGCCAGCC 1308
 QY 413 ArgAsnAlaGluGluGluGluPheValLeuLeuThrLeuArgGlyValLeuGluAsnGlu 432
 DB 1309 TTGCAGGAGGACTCTGGCACCCTACGTCTGCACACTAGATAAATGCTTCTTACTGTGACAAA 1368
 QY 433 PheGlyTyrLysLeuCysIlePheAspArgAspSerLeuProGlyGlyAsnThrValGlu 452
 DB 1369 ATGTCCATTGAGCTCAGAGTTTTTGAG-----AATACA---GAT 1404
 QY 453 AlaValPheAspPheIleGlnArgSerArgMetIle-----ValVal 467
 DB 1405 GCTTCTCTGCGGTTCACTCATACCCGCAAAATTTTAACCTTGTCAACCTCTGGGGTATTA 1464
 QY 468 LeuSerProAspTyrValThrGluLysSerIleSerMetLeuGluPheLysLeuGlyVal 487
 DB 1465 GTATGCCCTGAC-----CTGAGTGAATTC----- 1488
 QY 488 MetCysGlnAsnSerIleAlaThrLysLeuIleValValGluTyrArgProLeuGluHis 507
 DB 1489 -----ACCCGTGACAAAACCTGACGTGAAGATTCATGGGTACAAG----- 1527
 QY 508 ProHisProGlyIleLeuGlnLeuLysGluSerValSerPheValSerTrpLysGlyGlu 527
 DB 1528 -----GATTCTCTCTTTGGATAAAGACAAATGAGAAATTTCTTAAGTGTGAGGGGACC 1581
 QY 528 LysSer----- 529
 DB 1582 ACTCACTTACTCGTACACGATGTGGCCCTGGAAGATGCTGGCTATTACCGCTGTGCTGT 1641
 QY 530 -----LysHisSerGlySerLysPhe-----TrpLysAlaLeuArgLeuAlaLeu--- 544
 DB 1642 ACATTTCCCATGTAAGCCAGCAATACATCACTAGGAGTATTGAGTACGATCAAG 1701
 QY 545 -----ProLeuArgSerLeuSerAlaSer 552

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Db 1702 AAAAAAAAAAGAGAGACCATTCCTGTGATCATTTCCCTCCCTCAAGACCATATACAGTTCT 1761
Qy 553 SerGlyTrpAenGluSerCysSerSerGlnSerAspIleSerLeuAepHisValGlnArg 572
Db 1762 CTGGGG-----TCAAG-ACTGACAAATCCCATGTAAGGTGTTCTCTGGG 1802
Qy 573 ArgArgSerArgLeuLysGluProProGluLeuLysSer-----Glu 587
Db 1803 AACCGGCACACCCCTTAACCAACCATGCTGTGTGGAGCGGCCAATGACACCCACATAGAGAG 1862
Qy 588 ArgAlaAlaGlySerPro-----ProAlaProGly***MetSerLys----- 601
Db 1863 CGCTACCGGGAGCGCGTGCACGAGGGGCCACGCGCAAGATATTCAGAAAATATGA 1922
Qy 602 -----HisArgGlyLysSerSerAla 608
Db 1923 GAACATACATTGAAGTGCATTGATTTTGTATCTCTGTGCACAGAGAGATTTCACATGGA 1982
Qy 609 ThrCysArgCysCysValThrTyrCysGluGlyGluAsnHisLeuArgAsnLysSerArg 628
Db 1983 TTTTAAATGTGTGTCATATACCTCGAGTT- TTCAGACACACTACGCCACACAGTCAAGG 2041
Qy 629 AlaGluIleHisAenGlnProGlnTrpGluThrHisLeuCysLysProValProGlnGlu 648
Db 2042 -----AAGCCTCTCCACGT--- 2056
Qy 649 SerGluThrGlnTrpIleGlnAenGlyThrArgLeuGluProProAlaProGlnIleSer 668
Db 2057 -----TCTCCGGAGAGTCCAAATACGGTC 2080
Qy 669 AlaLeuAlaLeuHisHisPheThrAspLeuSerAsnAsnAsp 683
Db 2081 CGCCATGCC---CATCATGCCACACCTGAGTTCCTGGGGGGAC 2122
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RESULT 13

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US-10-282-162-55
; Sequence 55. Application US/10282162
; Publication No. US20030143697A1
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; TITLE OF INVENTION: AND USING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282,162
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 55
; LENGTH: 2754
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-282-162-55
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Alignment Scores:

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Pred. No.: 9.49e-214 Length: 2754
Score: 1937.50 Matches: 432
Percent Similarity: 62.06% Conservative: 49
Best Local Similarity: 55.74% Mismatches: 135
Query Match: 52.81% Indels: 161
DB: Gaps: 20
```

US-10-061-727-2 (1-687) x US-10-282-162-55 (1-2754)

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Qy 1 MetThrLeuLeuTrpCysValValSerLeuTyrPheTyrGlyIleLeuGlnSerAspAla 20
Db 1 ATGGTGCTCTGTGGTGTGTAGTGAGTCTCTACTTTTATGGAATCTCTGCAAGATGATGCC 60
Qy 21 SerGluArgCysAspAspTrpGlyLeuAspThrMetArgGlnIleGlnValPheGluAsp 40
```

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Db 61 TCAGAACGGCTGCCATGACTGGGAGCTAGACACCATAGAGCAAAATCCAAGTGTGTTGAAGAT 120
Qy 41 GluProAlaArgIleLysCysProLeuPheGluHisPheLeuLysPheAsnTyrSerThr 60
Db 121 GAGCCAGCTCGCATCAAGTCCACACTCTTTGAACACTTCTTTGAAATTTCAACTACAGACACA 180
Qy 61 AlaHisSerAlaGlyLeuThrLeuIleTyrTrpThrArgGlnAspArgAspLeuGlu 80
Db 181 GCCCATTCAGCTGGCTTACTCTGATCTGTGATTGGACTAGGAGGAGCCGAGACCTTTGAG 240
Qy 81 GluProIleAenPheArgLeuProGluAenArgIleSerLysGluLysAspValLeuTrp 100
Db 241 GAGCCAAATTAACCTTCGCTCCCGAGAACCGCATTTAGTAAGGAGAAAGATGTCTGTGG 300
Qy 101 PheArgProThrLeuLeuAenAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThr 120
Db 301 TTCGGGCCCACTCTCTCTCAATGACACTGGCAACTATACCTGCGATTTAAGNACACTACA 360
Qy 121 TyrCysSerLysValAlaPheProLeuGluValValGlnLysAspSerCysPheAsnSer 140
Db 361 TATTGAGCAAAAGTTTCCATTTCCTTTGGAAGTTGTTCAAAAAGACAGCTGTTTCAATTCC 420
Qy 141 ProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArgIleThrCys 160
Db 421 CCCATGAACCTCCAGTGCATAAATCTATATAGAATATGGCAATTCAGAGGATCACTTGT 480
Qy 161 ProAsnValAspGlyTyrPheProSerSerValLysProThrIleThrTyrTrpTyrMetGly 180
Db 481 CCAAAATGATGATGATATTTCTTCCAGTGTCAAACCGACTATCACTTGTGTATATGGGC 540
Qy 181 CysTyrLysIleGlnAsnPheAenAsnValIleProGluGlyMetAenLeuSerPheLeu 200
Db 541 TGTATATAAAATACAGAAATTTTATAATGTAATACCGAAGGTATGAATTTGAGTTTCCCTC 600
Qy 201 IleAlaLeuIleSerAenGlyAsnTyrThrCysValValThrTyrProGluAenGly 220
Db 601 ATTGCCTTTAATTTCAAATTAATGGAATTTACACATGTGTGTTACATATATCCAGAAATATGA 660
Qy 221 ArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProLysAsnAla 240
Db 661 CGTACGCTTTCATCTCACAGGAGCTCTGACTGTTAAGAGTAGTAGCTCTCCAAAAATATGCA 720
Qy 241 ValProProValIleHisSerProAsnAspHisValValTyrGluLysGluProGlyGlu 260
Db 721 GTGCCCTCTGTGATCCATTACCTAATGATCATGTGCTCTATGAGAAAGAACACGAGAGAG 780
Qy 261 GluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAspSerArgAsnGluVal 280
Db 781 GAGCTACTCATTCCTCTGAGGTCTATTTTATGTTTCTGATGATTTCTCGCAATGAGTTT 840
Qy 281 TrpTrpThrIleAspGlyLysLysProAspAspIleThrIleAspValThrIleAsnGlu 300
Db 841 TGGTGACCATTTGATGAAAAAAACCTGATGACATCACTATTGATGTCCACCATTAACGAA 900
Qy 301 SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLysLys 320
Db 901 AGTATAAGTCATAGTAGAAGATGAACAAAGAACTCAGATTTTGTAGCATCAAGAAA 960
Qy 321 ValThrSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAlaLysGlyGlu 340
Db 961 GTTACCTCTGAGGATCTCAAGCGCAGCTATGCTGTCATGCTAGAGTGCCTCAAGGCGAA 1020
Qy 341 ValAlaLysAlaAlaLysValLysGlnLysValProAlaProArgTyrThrValGluLeu 360
Db 1021 GTTGCCAAAGCAGCCAAAGGTGAAGCAGAAAGTGCCAGCTCCAAGATACACAGTGACACA 1080
Qy 361 -----AlaCysGlyPhe----- 364
Db 1081 GGGGCTGCCAGAAAGCTGCCGGTTCGTGGGAGGCATTACAAGCGGAGTTTCAGGCTGGAA 1140
Qy 365 GlyAlaThrValLeuLeuValValIleLeuIleValValTyrHisValTyrTrpLeuGlu 384
Db 1141 GGGGAGCTGTAGCCTGAGGTGCCCGCCAGGTG-----CCCTACTGTTGTGG 1188
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QY 201 ileAlaLeuileSerAsnAsnGlyAsnTyrThrCysValValThrTyrProGluAsnGly 220
Db 601 ATTGCCTTAAATTCAAATAATGGAAATACACATGTGTGTGTATACATATCCAGAAATATGGA 660
QY 221 ArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProLysAsnAla 240
Db 661 CGTAGGTTTCATCTCACAGGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAATAATGCA 720
QY 241 ValProProValIleHisSerProAsnAspHisValValTyrGluLysGluProGlyGlu 260
Db 721 GTGCCCCCTGTGTATCCATCACTAATGATCATGTGTCTATGAGAAAGAACACAGGAGAG 780
QY 261 GluLeuLeuileProCysThrValTyrPheSerPheLeuMetAspSerArgAsnGluVal 280
Db 781 GAGTACTCATCTCCCTGTACGGTCTATTATTAGTTTCTGATGGATTCTCGCAATGAGGTT 840
QY 281 TrpTrpThrIleAspGlyLysLysProAspAspileThrIleAspValThrIleAsnGlu 300
Db 841 TGGTGGACCATTTGATGGAAAAACCTGATGACATCACTATTGATGTACCATTTAACGAA 900
QY 301 SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLysLys 320
Db 901 AGTATAAGTCATAGACAGAAAGATGAAACAAAGAACTCAGATTTCGAGCATCAAGAAA 960
QY 321 ValThrSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAlaLysGlyGlu 340
Db 961 GTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTCATGCTAGAAGTGCNAAGGCGAA 1020
QY 341 ValAlaLysAlaAlaLysValLysGlnLysValProAlaProArgTyrThrValGluLeu 360
Db 1021 GTTGCCAAAGCAGCAGGAGTGAGCAGCAAGAGTGCCAGCTCCAGATACACAGTGACACA 1080
QY 361 -----AlaCysGlyPhe----- 364
Db 1081 GGGGCTGCCAAGACTGCCGTTTCGTGGGAGGCATTACAAGCGGGAGTTTCAGGCTGGAA 1140
QY 365 GlyAlaThrValLeuLeuValIleLeuIleValValTyrHisValTyrTrpLeuGlu 384
Db 1141 GGGAGGCTGTAGCCCTGAGGTGCCCGCCAGGTG-----CCCTACTGGTTGTGG 1188
QY 385 MetValLeuPheTyrArgAlaHisPhe----- 393
Db 1189 GCCTCTGTACGCCCCGCATCACTGACATGGCATGCAATAAATGACTCTGTAGACGGTC 1248
QY 394 ---GlyThrAspGluThrIleLeuAspGlyLysGluTyrAspIleTyrValSerTyrAla 412
Db 1249 CCAGGAGAAGAAGACAGACCGATGTGGCCCGCAGGCGGTGCTCTGTGGCTTCTGCCAGCC 1308
QY 413 ArgAsnAlaGluGluGluGluPheValLeuLeuThrLeuArgGlyValLeuGluAsnGlu 432
Db 1309 TTGCAGGAGGACTTGGCACCCTAGCTGCACTACTAGAAATGCTCTTACTGTGACAA 1368
QY 433 PheGlyTyrLysLeuCysIlePheAspArgAspSerLeuProGlyGlyAsnThrValGlu 452
Db 1369 ATGTCCATTGAGTCAGATTTTIGAG-----AATACA---GAT 1404
QY 453 AlaValPheAspPheIleGlnArgSerArgMetIle-----ValVal 467
Db 1405 GCITTCCTGCGGTTCATCTCATACCCGCAAAATTTAACTTGTCAACCTCTCGGGGTATTA 1464
QY 468 LeuSerProAspTyrValThrGluLysSerIleSerMetLeuLeuGluPheLysLeuGlyVal 487
Db 1465 GTATGCCCTGAC-----CTGAGTGAATTC----- 1488
QY 488 MetCysGlnAsnSerIleAlaThrLysLeuIleValValGluTyrArgProLeuGluHis 507
Db 1489 -----ACCCGTGACAAAATCTGAGTGAAGATTCAATGGTACAG----- 1527
QY 508 ProHisProGlyIleLeuGlnLeuLysGluSerValSerPheValSerTrpLysGlyGlu 527
Db 1528 -----GATTCTCTCTTTGGTATAAAGACAATGAGAAATTTCTTAAGTGTGAGGGGACC 1581

QY 528 LysSer----- 529
Db 1582 ACTCACTTACTCGPACAGATGTGGCCCTGGAAAGATCTGGCTATTACCGCTGTCTCTG 1641
QY 530 -----LysHisSerGlySerLysPhe-----TrpLysAlaLeuArgLeuAlaLeu--- 544
Db 1642 ACATTTCCTCCATGAGCCAGCAATACAACATCACTAGGAGTATTGAGCTACGATCAAG 1701
QY 545 -----ProLeuArgSerLeuSerAlaSer 552
Db 1702 AAAAAAAGAGAGACCATTCCTGTGATCATTTCCCCCTCAAGACCATATCAGTTCT 1761
QY 553 SerGlyTrpAsnGluSerCysSerSerGlnSerAspIleSerLeuAspHisValGlnArg 572
Db 1762 CTGGGG-----TCAAG-ACTGACAAATCCCATGTAAGGTGTTTCTGGG 1802
QY 573 ArgArgSerArgLeuLysGluProProGluGlnSerSer-----Glu 587
Db 1803 AACGGGCACACCTTAACCACTATGCTGTGTGGAGCGGCCAATGACACCCACATAGAGAG 1862
QY 588 ArgAlaAlaGlySerPro-----ProAlaProGly***MetSerLys----- 601
Db 1863 CGCCTACCGGGAGCGCGCTGACCGAGGGGCCAGCGAATATTTCAGAAAATAATGA 1922
QY 602 -----HisArgGlyLysSerSerAla 608
Db 1923 GAACATCAATTGAAGTGCATTGATTTTGTATCTCTGCACAGAGAGGATTTGCACATGGA 1982
QY 609 ThrCysArgCysCysValThrTyrCysGluGlyGluAsnHisLeuArgAsnLysSerArg 628
Db 1983 TTTTAATGTGTGTCTCCATTAATACCTGAGTTTTCAGACACTACGCACACCATCAAGG 2041
QY 629 AlaGluIleHisAsnGlnProGlnTrpGluThrHisLeuCysLysProValProGlnGlu 648
Db 2042 -----AAGCCTCTCCACGT--- 2056
QY 649 SerGluThrGlnTrpIleGlnAsnGlyThrArgLeuGluProProAlaProGlnIleSer 668
Db 2057 -----TCTCCGGAGAGTCCCAATACGGTC 2080
QY 669 AlaLeuAlaLeuHisPheThrAspLeuSerAsnAsnAsp 683
Db 2081 CGCCATGCC---CATCATGCCAGCACCTGAGTTCTTGGGGGGAC 2122
RESULT 15
US-10-840-138-25
; Sequence 25, Application US/10840138
; Publication No. US20040224893A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Li-Hsien
; APPLICANT: Lin, Hsin Chieh
; APPLICANT: Karow, Margaret
; TITLE OF INVENTION: Methods of Using IL-1 Antagonists to Treat Neointimal Hyperplasia
; FILE REFERENCE: REG 207A
; CURRENT APPLICATION NUMBER: US/10/840,138
; CURRENT FILING DATE: 2004-05-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 2754
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-840-138-25
Alignment Scores:
Pred. No.: 9,49e-214 Length: 2754
Score: 1937.50 Matches: 432
Percent Similarity: 62.06% Conservative: 49
Best Local Similarity: 55.74% Mismatches: 135
Query Match: 52.81% Indels: 161
DB: 8 Gaps: 20
US-10-061-727-2 (1-687) x US-10-840-138-25 (1-2754)

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 1 ATGGTGTCTCTGTGTGTGTAGTGTAGTCTCTACTTTATGGAAATCTCTGCAAGTGTATGCC 60
 21 SerGluArgCysAspAspTrpGlyLeuAspThrMetArgGlnIleGlnValPheGluAsp 40
 61 TCAGAACGCTGCGATGACTGGGAGCTAGACACCATGAGGCAAAATCCAAGTGTTCAGAGAT 120
 41 GluProAlaArgIleIleCysProLeuPheGluHisPheLeuLysPheAsnTyrSerThr 60
 121 GAGCAGCTCGCATCAAGTGCACCTCTTTGAACACTCTCTTCAAAATTTCAACTACAGCACA 180
 61 AlaHisSerAlaGlyLeuThrLeuIleTrpTyrTrpThrArgGlnAspArgAspLeuGlu 80
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 121 TyrCysSerLysValAlaPheProLeuGluValValGlnLysAspSerCysPheAsnSer 140
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 481 CCAAAATAGATGGATATTTCTTCCAGTGTCAAAACCGACTATCACTTGGTATATGGGC 540
 181 CysTyrValIleGlnAsnPheAsnValIleProGluGlyMetAsnLeuSerPheLeu 200
 541 TGTATATAAATACAGAAATTTAATATGTAATACCCGAGGATGAATCTGAGTGTCTC 600
 201 IleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValThrTyrProGluAsnGly 220
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 661 CGTAGCTTTCATCTCACCAGGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAAAATGCA 720
 241 ValProValIleHisSerProAsnAspHisValValThrGluLysGluProGlyGlu 260
 721 GTGCCCCCTGTGATCCATTCACCTAATGATCATGTGGTCTATGAGAAAGAACCCAGAGAG 780
 261 GluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAspSerArgAsnGluVal 280
 781 GAGCTACTCATTCCTGTACGGTCTATTTAGTTTCTGATGGATTCCTCGCAATGAGGT 840
 281 TrpTrpThrIleAspGlyLysLysProAspAspIleThrIleAspValThrIleAsnGlu 300
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 301 SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLysLys 320
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 321 ValThrSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAlaLysGlyGlu 340
 961 GTTACTCTGAGGATCTCAAGCGCAGCTATGTCTGTCTGATGTAGTAAGTGCACAAAGCCGA 1020
 341 ValAlaLysAlaLysValLysGlnLysValProAlaProArgTyrThrValGluLeu 360
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361 QY -----AlaCysGlyPhe----- 364
 1081 DB GGGGCTGCCAAGAGCTGCGGTTCGTGGGAGGCATTACAAGCGGAGTTTCAGGTGGNA 1140
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 1141 DB GGGGAGCGCTGTAGCCTGAGGTGCGCCCGAGGTG-----CCCTACTGTTGTGG 1188
 385 QY MetValLeuPheTyrArgAlaHisPhe----- 393
 1189 DB GCCTGTGTACGCCCCCGCATCAACCTGACATGGCATATAAAATGACTCTGTAGTAGCGTTC 1248
 394 QY ---GlyThrAspGluThrIleLeuAspGlyLysGluTyrAspIleTyrValSerTyrAla 412
 1249 DB CCAGGAGGAAGAGACACGAGTGTGGGCCAGGACGGTCTCTGTGGCTTCGCCAGCC 1308
 413 QY ArgAsnAlaGluGluGluPheValLeuLeuThrLeuArgGlyValLeuGluAsnGlu 432
 1309 DB TTGCAGGAGGACTCTGGCACCTAGCTCTGCACACTAGAAAATGCTTCTTACTGTGACAAA 1368
 433 QY PheGlyTyrLysLeuCysIlePheAspArgAspSerLeuProGlyGlyAsnThrValGlu 452
 1369 DB ATGTCCATTGAGCTCAGAGTTCAG-----AATACA---GAT 1404
 453 QY AlaValPheAspPheIleGlnArgSerArgArgMetIle-----ValVal 467
 1405 DB GCTTCTGCGGTTCATCTCATACCGCAATTTTAACCTTGTCAACCTCTGGGGTATTA 1464
 468 QY LeuSerProAspTyrValThrGluLysSerIleSerMetLeuGluPheLysLeuGlyVal 487
 1465 DB GTATGCCCTGAC-----CTGATGAATTC----- 1488
 488 QY MetCysGlnAsnSerIleAlaThrLysLeuIleValValGluTyrArgProLeuGluHis 507
 1489 DB -----ACCCGTGACAAAACCTGACGTGAAGATTCAAATCGTCAAG----- 1527
 508 QY ProHisProGlyIleLeuGlnLysGluSerValSerPheValSerTrpLysGlyGlu 527
 1528 DB -----GATTCCTCTTTTGGATAAAGCAATGAGAAATTTCTAAGTGTGAGGGGGACC 1581
 528 QY LysSer----- 529
 1582 DB ACTCACTTACTCGTACAGATGTGCCCTCGGAGATGTGGCTATTACCGCTGTCTCCTG 1641
 530 QY -----LysHisSerGlySerLysPhe-----TrpLysAlaLeuArgLeuAlaLeu--- 544
 1642 DB ACATTTGCCCATGAAGGCCAGCAATACAACTACATCACTAGGATATTGAGCTACGCATCAAG 1701
 545 QY -----ProLeuArgSerLeuSerAlaSer 552
 1702 DB AAAAAAAGAGAGAGACCATTCCTGTGATCATTTCCCTCCCTCAAGACCATATCAGCTTCT 1761
 553 QY SerGlyTrpAsnGluSerCysSerSerGlnSerAspIleSerLeuAspHisValGlnArg 572
 1762 DB CTGGGG-----TCAAG-ACTGACAATCCCATGTAAGGTGTTTCTGGG 1802
 573 QY ArgArgSerArgLeuLysGluProProGluLeuGlnSerSer-----Glu 587
 1803 DB AACCGGCACACCTTAAACCAACCATGCTGTGTGGACGGCCCAATGACACCCACATAGAGAG 1862
 588 QY ArgAlaAlaGlySerPro-----ProAlaProGly***MetSerLys----- 601
 1863 DB CGCTACCGGGGCGCGGTGACCGAGGGGCCAGCCGAGGAATATTTCAGAAAATAATAGA 1922
 602 QY -----HisArgGlyLysSerSerAla 608
 1923 DB GAACCTATTGAAGTGCATTGATTTTGTATCTCTGTACAGAGAGAGGATTTTGCACATGGA 1982
 609 QY ThrCysArgCysValThrTyrCysGluGlyGluAsnHisLeuArgAsnLysSerArg 628
 1983 DB TTTTAAATGTGTTGTTCCATAATACCTCAGTTT-TTCAGACACTACGACACCACTCAGG 2041
 629 QY AlaGluIleHisAsnGlnProGlnTrpGluThrHisLeuCysLysProValProGluGlu 648

Db	2042	-----			----	2056
Qy	649	SerGluThrGlnTrpIleGlnAsnGlyThrArgLeuGluProProAlaProGlnIleSer	----	-----	-----	668
Db	2057	-----		----	-----	2080
Qy	669	AlaLeuAlaLeuHisPheThrAspLeuSerAsnAsnAsnLeu	----	-----	-----	683
Db	2081	CGCATGCC---			----	2122
		---CACCATGCCACACCTGAGTTCTCGGGGGGAC	----	-----	-----	

Search completed: December 14, 2005, 18:39:24
Job time : 1461 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 14, 2005, 15:34:05 ; Search time 209 Seconds
(without alignment)

1611.180 Million cell updates/sec

Title: US-10-061-727-2

Perfect score: 3669

Sequence: 1 MTLWCVVSLVFGILQSDA.....SALAHHTDLSNNDFYIL 687

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4161359 seqs, 245077644 residues

Total number of hits satisfying chosen parameters: 8322718

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US10061727/runat_07122005_113339_17291/app_query.fasta_1.839
-DB=Published Applications NA New -QFMT=fastap -SUFFIX=sp2n.rnpbn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10061727@cgn1_1_148@runat_07122005_113339_17291
-NCPU=6 -ICPU=3 -NO_WMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSBBLCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARGEN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA_New.*

1: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
5: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
6: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1938	52.8	2748	7	US-11-144-987-21
2	1937.5	52.8	2754	7	US-11-144-987-23
3	1937.5	52.8	2754	7	US-11-144-987-25
4	1935	52.7	2703	7	US-11-144-987-9
5	1935	52.7	2709	7	US-11-144-987-11
6	1935	52.7	2709	7	US-11-144-987-13
7	1930	52.6	2733	7	US-11-144-987-1
8	1833	50.0	2703	7	US-11-144-987-3

Alignment Scores:			
Pred. No.:	3.1e-184	Length:	2748
Score:	1938.00	Matches:	432
Percent Similarity:	63.42%	Conservative:	50
Best Local Similarity:	56.84%	Mismatches:	141
Query Match:	52.82%	Indels:	140
DB:	7	Gaps:	19

US-10-061-727-2 (1-687) x US-11-144-987-21 (1-2748)

ALIGNMENTS

RESULT 1

US-11-144-987-21

; Sequence 21, Application US/11144987

; Publication No. US2005027655A1

; GENERAL INFORMATION:

; APPLICANT: Mellis, Scott

; APPLICANT: Karow, Margaret

; APPLICANT: Yancopoulos, George

; APPLICANT: Papadopoulos, Joanne

; TITLE OF INVENTION: Methods of Using IL-1 Antagonists to Treat Autoinflammatory Disease

; FILE REFERENCE: REG 2090A

; CURRENT APPLICATION NUMBER: US/11/144,987

; PRIOR FILING DATE: 2005-06-03

; PRIOR FILING DATE: 2004-06-04

; NUMBER OF SEQ ID NOS: 26

; SOFTWARE: FASTSEQ for Windows Version 3.0

; SEQ ID NO 21

; LENGTH: 2748

; TYPE: DNA

; ORGANISM: Homo sapiens

US-11-144-987-21

Sequence 5, Appl
Sequence 7, Appl
Sequence 17, Appl
Sequence 19, Appl
Sequence 15, Appl
Sequence 365, App
Sequence 367, App
Sequence 371, App
Sequence 48357, A
Sequence 366, App
Sequence 437, App
Sequence 13344, A
Sequence 6, Appl
Sequence 13479, A
Sequence 48351, A
Sequence 357, App
Sequence 770, App
Sequence 13313, A
Sequence 303, App
Sequence 9887, Ap
Sequence 456, App
Sequence 357, App
Sequence 358, App
Sequence 312, App
Sequence 1311, A
Sequence 155, App
Sequence 154, App
Sequence 153, App
Sequence 12, Appl
Sequence 13, Appl
Sequence 351, App
Sequence 388, App
Sequence 387, App
Sequence 783, App
Sequence 389, App
Sequence 14, Appl

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Dbb 1 ATGGTGCTCTCTGTGTGTAGTGAAGTCTTATGGAATCCTGCAAGTGTATGCC 60
Qy 21 SerGluArgCysAspAspTrpGlyLeuAspThrMetArgGlnIleGlnValPheGluAsp 40
Dbb 61 TCAGAACGCTCGATGACTGGGGACTAGACACCATGAGGCAAAATCCAAAGTGTTTGAAGAT 120
Qy 41 GluProAlaArgIleLysCysProLeuPheGluHisPheLeuLysPheAsnTyrSerThr 60
Dbb 121 GAGCAGCTGCATCAAGTGCCTCTTTGAAACACTTCTTGAATTCACACTACAGACACA 180
Qy 61 AlahisSerAlaGlyLeuThrLeuIleTrpTyrTrpThrArgGlnAspArgAspLeuGlu 80
Dbb 181 GCCCATTTTCAGTGCCCTTACTCTGATCTGGTATTGGACTAGGCAGGACCGGACCTTGAG 240
Qy 81 GluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTrp 100
Dbb 241 GAGCCAAITTAATTCGCCCTCCCCGAGAACCGCAATTAGTAAGGAGAAAGATGTCTGTGG 300
Qy 101 PheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThr 120
Dbb 301 TTCGGGCCACTCTCTCCTCAATGACACTGSCAACTATACCTGCATGTTAAGGAACACTACA 360
Qy 121 TyrCysSerLysValAlaPheProLeuGluValValGlnLysAspSerCysPheAsnSer 140
Dbb 361 TATTGCAAGCAAGTGCATTTCCCTTGGAAAGTTGTTCAAAAAGACAGCTGTTTCAATTC 420
Qy 141 ProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArgIleThrCys 160
Dbb 421 CCCATGAACCTCCAGTGCATAAATCTATATAGATATGGCAATTCAGAGGATCAGTTGT 480
Qy 161 ProAsnValAspGlyTyrPheProSerSerValLysProThrIleThrTrpTyrMetGly 180
Dbb 481 CCAATGTAGATGATATTTCTTCCAGTGTCAAACCGACTATCATTCTGTATATGGGC 540
Qy 181 CysTyrLysIleGlnAsnPheAsnAsnValIleProGluGlyMetAsnLeuSerPheLeu 200
Dbb 541 TGTATATAAATACAGAAATTTAATAATGTAATACCCGAAGGTATGAATTTGAGTTTCCCTC 600
Qy 201 IleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValThrTyrProGluAsnGly 220
Dbb 601 ATTGCCCTTAATTTCAAATAATAGAAATTTACATATGTTGTATACATATCCAGAAATGGA 660
Qy 221 ArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProLysAsnAla 240
Dbb 661 CGTAGGTTTCATCTCACCGAGACTCTGACTGTAAAGTAGTAGGCCTCTCCAAAATGCA 720
Qy 241 ValProProValIleHisSerProAsnAspHisValValTyrGluLysGluProGlyGlu 260
Dbb 721 GTGCCCTCTGTATCCATTACCTAATATGATCATGTGTTGTATGAGAAAGAACCCAGGAGAG 780
Qy 261 GluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAspSerArgAsnGluVal 280
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Qy 281 TrpTrpThrIleAspGlyLysLysProAspAspIleThrIleAspValThrIleAsnGlu 300
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Qy 321 ValThrSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAlaLysGlyGlu 340
Dbb 961 GTTACCTCTGAGGATCTCAAGCCGAGCTATGTCTGTCATGCTAGAAAGTGCAGAAAGCGAA 1020
Qy 341 ValAlaLysAlaLysValLysGlnLysValProAlaProArgTyrThrValGluLeu 360
Dbb 1021 GTTGCCCAAGACGCAAGGTGAAGAGAAAGTCCAGCTCCAGATACACAGTGCACACA 1080

Qy 361 -----AlaCysGlyPhe----- 364
Dbb 1081 GGGGCTGCCAGAAAGCTGCCGGTTTCGTGGGAGGCATTACAAGCGGGAGTTTCAGGCTGGAA 1140
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Dbb 1141 GGGAGGCTTAGCCCTGAGGTGCCCGCCAGGTG-----CCCTACTGTTGTGG 1188
Qy 385 MetValLeuPheTyrArgAlaHisPhe----- 393
Dbb 1189 GCCTCTGTAGCCCCCGCATCAACCTGACATGCATATAAAATGACTCTGTAGACCGTC 1248
Qy 394 ---GlyThrAspGluThrIleLeuAspGlyLysGluTyrAspIleTyrValSerTyrAla 412
Dbb 1249 CCAGGAGAAAGAGACACCGATGTGGCCCGAGCGGTCTCTGTGGCTTCTGCCAGCC 1308
Qy 413 ArgAsnAlaGluGluGluGluPheValLeuLeuThrLeuArgGlyValLeuGluAsnGlu 432
Dbb 1309 TTGCAGGAGGACTCTGGCACTACGTCTGCACCTAGATAAATGCTTCTTACTGTGCAAA 1368
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Dbb 1528 -----GATTCCTCTCTTTGGATAAAGACAATGAGAAATTTCTAAGTGTGAGGGGACC 1581
Qy 528 LysSer----- 529
Dbb 1582 ACTCACTTACTCTACACGATGTGGCCCTGGAAAGATGCTGGCTATTACCGCTGTCTGTG 1641
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Qy 545 -----ProLeuArgSerLeuSerAlaSer 552
Dbb 1702 AAAAAAAGAGAGAGACCATTCCTGTGATCATTTCCCGCTCAAGACCATATCAGCTTCT 1761
Qy 553 SerGlyTyrAsnGluSerCysSerSerGlnSerAspIleSerLeuAspHisValGlnArg 572
Dbb 1762 CTGGGG-----TCAAG-ACTGACAATCCCATGTAAGTGTCTCTGGG 1802
Qy 573 ArgArgSerArgLeuLysGluProProGluLeuGlnSerSer-----Glu 587
Dbb 1803 AACCGGCACACCTTAAACCCACCATGCTGTGTGGAGCGGCNAATGACCCACACATAGAGAG 1862
Qy 588 ArgAlaAlaGlySerPro-----ProAlaProGly***MetSerLys----- 601
Dbb 1863 CGCTACCCGGAGGCGCGGTGACCGAGGGGCCCGCAGGAATAATTCAGAAAAATAATGA 1922
Qy 602 -----HisArgGlyLysSerSerAla 608
Dbb 1923 GAACATACATTGAAGTCCCATTTGATTTTGTCTCTGTCAAGAGAGGATTTGCACATGGA 1982
Qy 609 ThrCysArgCysCysValThrTyrCysGluGlyGluAsnHisLeuArgAsnLysSerArg 628
Dbb 1983 TTTTAAATGTGTGTCCATAATACCTCTGAGTT-TTCAGACACTTACCGCACACAGTCAAGG 2041
Qy 629 AlaGluIleHisAsnGlnProGlnTrpGluThrHisLeuCysLysProValProGlnGlu 648


```
Db 2042 AAGCCTCCTCCAGTTCTCCGAGAC-AAAACTCACACATGCCACCGTCCGACCACT 2100
Qy 649 SerGluThrGlnTrpIleGlnAsnGlyThrArg-----LeuGluProProAlaProGln 666
Db 2101 GAA-----CTCCTGGGGGACCGTCAGTCTTCTCTTCCCTCCCAAAACCCCAAG 2148

RESULT 2
US-11-144-987-23
; Sequence 23, Application US/11144987
; Publication No. US2005027265A1
; GENERAL INFORMATION:
; APPLICANT: Mellis, Scott
; APPLICANT: Karow, Margaret
; APPLICANT: Yancopoulos, George
; APPLICANT: Papadopoulos, Joanne
; TITLE OF INVENTION: Methods of Using IL-1 Antagonists to Treat Autoinflammatory Diseases
; FILE REFERENCE: REG 2090A
; CURRENT APPLICATION NUMBER: US/11/144,987
; PRIOR FILING DATE: 2005-06-03
; PRIOR FILING DATE: 60/577,023
; PRIOR FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 2754
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-144-987-23

Alignment Scores:
Pred. No.: 3,498-184 Length: 2754
Score: 1937.50 Matches: 432
Percent Similarity: 62.06% Conservative: 49
Best Local Similarity: 55.74% Mismatches: 135
Query Match: 52.81% Indels: 161
DB: 7 Gaps: 20

US-10-061-727-2 (1-687) x US-11-144-987-23 (1-2754)
Qy 1 MetThrLeuLeuTrpCysValValSerLeuTyrPheTyrGlyIleLeuGlnSerAspAla 20
Db 1 ATGGTGCTTCTGTGTGTAGTAGTCTCTACTTTTATGGAATCTCTCAAGATGATGCC 60
Qy 21 SerGluArgCysAspAspTrpGlyLeuAspThrMetArgGlnIleGlnValPheGluAsp 40
Db 61 TCAGAACCTCGCATGACTGGGGACTAGACACCATGAGGCAAAATCCAAAGTGTTTGAAGAT 120
Qy 41 GluProAlaArgIleLysCysProLeuPheGluHisPheLeuLysPheAsnTyrSerThr 60
Db 121 GAGCCAGCTCCGATCAAGTGGCCACTCTTTGAAACACTTCTTGAATTCNACTACAGACA 180
Qy 61 AlaHisSerAlaGlyLeuThrLeuIleTrpTyrTrpThrArgGlnAspArgAspLeuGlu 80
Db 181 GCCCATTCAGCTGGCTTACTCTGATCTGTGATTGGACTAGGACGAGCCGGACCTTGAG 240
Qy 81 GluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTrp 100
Db 241 GAGCAATTAATCTCCGCTCCCGAGAACCGCATTTAGTAAGGAAAGATGTCTGTGG 300
Qy 101 PheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThr 120
Db 301 TTCCGGCCCACTCTCTCAATGACACTGGCACTATACCTGCATGTTNAGGAAACACTACA 360
Qy 121 TyrCysSerLysValAlaPheProLeuGluValValGlnLysAspSerCysPheAsnSer 140
Db 361 TATTGCAGCAAGTTGCATTTCCCTTGAAGTGTGTTCAAAAAGACAGCTGTTTCAATTC 420
Qy 141 ProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArgIleThrCys 160
Db 421 CCCATGAACATCCCGATGTCATAAACTGTATAGAAATATGTCATTCAGAGATCACTGT 480
Qy 161 ProAsnValAspGlyTyrPheProSerSerValLysProThrIleThrTrpTyrMetGly 180
```

```
Db 481 CCAAATGTAGATGATATTTTCTTCCAGTGTCAAAACCGACTATCACATTGGTATATGGC 540
Qy 181 CysTyrLysIleGlnAsnPheAsnValIleProGluGlyMetAsnLeuSerPheLeu 200
Db 541 TGTATATAATACAGAAATTTTAAATATATACCCGAAGGTATGAACCTTGAGTTTCTC 600
Qy 201 IleAlaLeuLeuSerAsnAsnGlyAsnTyrThrCysValValThrTyrProGluAsnGly 220
Db 601 ATTGCTTTAATTTCAATATATGGAATTTACACATGTGTTGTATACATATCCAGAAAATGGA 660
Qy 221 ArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProLysAsnAla 240
Db 661 CGTACGTTTCACTCCACGAGACTCTGACTGAAGGTAGTAGGCTCTCCAAAAAATGCA 720
Qy 241 ValProProValIleHisSerProAsnAspHisValValTyrGluLysGluProGlyGlu 260
Db 721 GTGCCCCCTGTGATGCCATTCACCTAAATGATCATGTGCTATAGAAAGAACCCAGGAGAG 780
Qy 261 GluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAspSerArgAsnGluVal 280
Db 781 GAGCTACTCATTCCTGTACGGTCTATTTAGTTTTCTGATGGATTCTCGCAATGAGGTT 840
Qy 281 TrpTrpThrIleAspGlyLysLysProAspAspIleThrIleAspValThrIleAsnGlu 300
Db 841 TGGTGGACCATTTGATGAAAAAAACCTGATGACATCACTATTGATGTCAACATTAAACGAA 900
Qy 301 SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLysLys 320
Db 901 AGTATAAGTTCATAGTAGAAGAGATGAAACAAAGAACTCAAGATTTTGGAGATCAAGAAA 960
Qy 321 ValThrSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAlaLysGlyGlu 340
Db 961 GTTACCTCTGAGGATCTCAAGCGCAGCTATGCTGTCTATGCTAGAGTGCCAAAGCCGAA 1020
Qy 341 ValAlaLysAlaAlaLysValLysGlnLysValProAlaProArgTyrThrValGluLeu 360
Db 1021 GTTGCCAAAGCAGCCAAAGGTGAAGCAGAAAGTGCCAGCTCCCAAGATACACAGTGCACACA 1080
Qy 361 -----AlaCysGlyPhe----- 364
Db 1081 GGGGCTGCCAAGAGCTCCCGGTTTCTGGGGAGGCATTACAAGCGGGAGTTTCAGGCTGGAA 1140
Qy 365 GlyAlaThrValLeuLeuValValIleLeuIleValValTyrHisValTyrTrpLeuGlu 384
Db 1141 GGGGAGCTGTAGCCCTGAGGTGCCCGCCAGGTG-----CCCTACTGGTTGTGG 1188
Qy 385 MetValLeuPheTyrArgAlaHisPhe----- 393
Db 1189 GCCTCTGTACGCCCGCCGATCAACCTGACATGGCATAAAAATGACTCTGTCTAGGACGTC 1248
Qy 394 ---GlyThrAspGluThrIleLeuAspGlyLysGluTyrAspIleTyrValSerTyrAla 412
Db 1249 CCAGGAGAAGAAGACAGACACGATGTGGGCCCGAGCGGTGCTCTGTGGCTCTCTGCCAGCC 1308
Qy 413 ArgAsnAlaGluGluGluPheValLeuLeuThrLeuArgGlyValLeuGluAsnGlu 432
Db 1309 TTGCAGGAGGACTCTGGCAGCTACGCTGCACTACTAGAAATGCTCTTACTGTGACAAA 1368
Qy 433 PheGlyTyrLysLeuCysIlePheAspArgAspSerLeuProGlyGlyAsnThrValGlu 452
Db 1369 ATGTCCATTGAGCTCAGAGTTTGTAG-----AATACA--GAT 1404
Qy 453 AlaValPheAspPheIleGlnArgSerArgArgMetIle-----ValVal 467
Db 1405 GCTTTCCTGCGGTTTCATCTCATACCCGCAAAATTTAAACCTTGTCAACCTCTCGGGGTATA 1464
Qy 468 LeuSerProAspTyrValThrGluLysSerIleSerMetLeuGluPheLysLeuGlyVal 487
Db 1465 GTATGCCCTGAC-----CTGAGTGAATTC----- 1488
Qy 488 MetCysGlnAsnSerIleAlaThrLysLeuIleValValGluTyrArgProLeuGluHis 507
```

```
Db 1489 -----ACCGGTGACAAABACGCTGACGATTCATGGTACAAG----- 1527
Qy 508 ProHisProGlyIleLeuGlnLeuLysGluSerValSerPheValSerTrpLysGlyGlu 527
Db 1528 -----GATTCTCTTCTTTGGATAAAGACAATGAGAAATTTCTAAGTGTGAGGGGACC 1581
Qy 528 LysSer----- 529
Db 1592 ACTCACTTACTGCTACAGATGTGGCCCTGGAAGATGCTGGCTATTACCGCTGTGCTGTG 1641
Qy 530 -----LysHisSerGlySerLysPhe-----TrpLysAlaLeuArgLeuAlaLeu--- 544
Db 1642 ACATTGCGCCATGAAGGCGAGCAATACACATCACTAGGAGTATTGACCTACGATCAAG 1701
Qy 545 -----ProLeuArgSerLeuSerAlaSer 552
Db 1702 AAAAAAAGAGAGACCATTCCTGTGATCATTTCCCGCCCTCAAGACCATATCAGCTTCT 1761
Qy 553 SerGlyTrpAenGluSerCysSerSerGlnSerAspIleSerLeuAspHisValGlnArg 572
Db 1762 CTGGGG-----TCAAG-ActGACAAATCCCATGTAAGGTGTTTCTGGG 1802
Qy 573 ArgArgSerArgLeuLysGluProProGluLeuGlnSerSer-----Glu 587
Db 1803 AACCGGCACACCTTTAACCCATGCTGTGTGGAGCGGCCAATGACACCCACATAGAGAG 1862
Qy 588 ArgAlaAlaGlySerPro-----ProAlaProGly***MetSerLys----- 601
Db 1863 CGCTACTCCGGAGGCGCGGTGACCGAGGGGCCACGCGAGGAATATTGAGAAATAATGA 1922
Qy 602 -----HisArgGlyLysSerSerAla 608
Db 1923 GAATACATTGAAGTGCATTTGATTCCTGTCACAGAGGAGGATTTGCCATGGA 1982
Qy 609 ThrCysArgCysCysValThrTrpCysGlyGluAsnHisLeuArgAsnLysSerArg 628
Db 1983 TTTTAAATGTGTTCATATAACCTGAGTT-TTCAGACACTACGACACACAGTCAAGG 2041
Qy 629 AlaGluIleHisAenGlnProGlnTrpGluThrHisLeuCysLysProValProGlnGlu 648
Db 2042 -----AAGCCTCTCCACGT--- 2056
Qy 649 SerGluThrGlnTrpIleGlnAsnGlyThrArgLeuGluProProAlaProGlnIleSer 668
Db 2057 -----TCTCCGGAGAGTCCAAATACGGTC 2080
Qy 669 AlaLeuAlaLeuHisHisPheThrAspLeuSerAsnAsnAsp 683
Db 2081 CGCCATGCC---CATCATGCCACACCTGAGTTCTCTGGGGGAC 2122

RESULT 3
US-11-144-987-25
; Sequence 25, Application US/11144987
; Publication No. US20050272655A1
; GENERAL INFORMATION:
; APPLICANT: Mellis, Scott
; APPLICANT: Karow, Margaret
; APPLICANT: Yancopoulos, George
; APPLICANT: Papadopoulos, Joanne
; TITLE OF INVENTION: Methods of Using IL-1 Antagonists to Treat Autoinflammatory Disease
; FILE REFERENCE: REG 2090A
; CURRENT APPLICATION NUMBER: US/11/144,987
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: 60/577,023
; PRIOR FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 2754
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-144-987-25
```

Alignment Scores:

Pred. No.: 3,49e-184 Length: 2754
Score: 1937.50 Matches: 432
Percent Similarity: 62.06% Conservative: 49
Best Local Similarity: 55.74% Mismatches: 135
Query Match: 52.81% Indels: 161
DB: 7 Gaps: 20

US-10-061-727-2 (1-687) x US-11-144-987-25 (1-2754)

```
Qy 1 MetThrLeuLeuTrpCysValValSerLeuTyPheTyTrpGlyIleLeuGlnSerAspAla 20
Db 1 ATGTGTCTTCTGTGTGTGTAGTGTCTCTACTTTTATGGAATTCCTGCAAGTGTGATGCC 60
Qy 21 SerGluArgCysAspAspTrpGlyLeuAspThrMetArgGlnIleGlnValPheGluAsp 40
Db 61 TCAGAACGCTCGCATGACTGGGACTAGACACCATGAGGCAATCCAAGTGTTTGAAGAT 120
Qy 41 GluProAlaArgIleLysCysProLeuPheGluHisPheLeuLysPheAsnTySerThr 60
Db 121 GAGCCAGCTCGCATCAAGTGCCTCTCTTTGAACACTTCTTGAATTTCAACTACAGACA 180
Qy 61 AlaHisSerAlaGlyLeuThrLeuLeuTrpTyTrpThrArgGlnAspArgAspLeuGlu 80
Db 181 GCCATTTCAGTGGCTTCTCTGATCTGTATTGGACTAGGACGAGCCGGACCTTGGAG 240
Qy 81 GluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTrp 100
Db 241 GAGCCAAATTAACCTCCGCTCCCGAGAACCGCATTAGTAAGAGAAAGATGTCTGTGG 300
Qy 101 PheArgProThrLeuLeuAsnAspThrGlyAsnTyThrCysMetLeuArgAsnThrThr 120
Db 301 TTCGGGCCCACTCTCTCTCAATGACACTGCGCAACTATACCTGCTGATTTAAGGAACACTACA 360
Qy 121 TrpCysSerLysValAlaPheProLeuGluValValGlnLysAspSerCysPheAsnSer 140
Db 361 TATTGAGCAAAAGTGGATTTCCTTGGAAAGTTGTTCAAAAAGACAGCTGTGTTCAATTC 420
Qy 141 ProMetLysLeuProValHisLysLeuTyTrpIleGluTyTrpGlyIleGlnArgIleThrCys 160
Db 421 CCCATGAAACTCCAGTGCATAAATCTATATAGATATGCGCATTCAGAGATCACATTGT 480
Qy 161 ProAsnValAspGlyTyTrpPheProSerSerValLysProThrIleThrTrpTyMetGly 180
Db 481 CCAAAATGTAGATGGATATTTTCTTCCAGTGTCAAAACCGACTATCACTTGGTATATGGGC 540
Qy 181 CysTyTrpLysIleGlnAsnPheAsnValIleProGluGlyMetAsnLeuSerPheLeu 200
Db 541 TGTATAAANAATCAGAAATTTTAATAATGTAATACCCGGAAGGTATGAACCTTGAGTTTCCTC 600
Qy 201 IleAlaLeuIleSerAsnAsnGlyAsnTyThrCysValValThrTyTrpProGluAsnGly 220
Db 601 ATTGCCCTTAATTTCAATAATGAAATTTACACATGTGTTGTTACATATCCAGAAATGGA 660
Qy 221 ArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProLysAsnAla 240
Db 661 CGTACGTTTTTCATCTCACAGGACTCTGACTGTGAAGGTAGTAGGCTCTCCAAAAAATGCA 720
Qy 241 ValProProValIleHisSerProAsnAspHisValValTyTrpGluLysGluProGlyGlu 260
Db 721 GTGCCCCCTGTGATCTCATTTACCTAATGATCATGTGCTTATGAGAAAGAACACGAGAG 780
Qy 261 GluLeuLeuIleProCysThrValTyTrpPheSerPheLeuMetAspSerArgAsnGluVal 280
Db 781 GAGTACTCATTCCTCTGACGGTCTATTTTAGTTTCTGATGATCTCTCGCAATGAGTT 840
Qy 281 TrpTrpThrIleAspGlyLysLysProAspAspIleThrIleAspValThrIleAsnGlu 300
Db 841 TGTGTGACCATTTGATGAAAAAACCCTGATGACATCACTATTGATGTCCACCATTAACGAA 900
Qy 301 SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLys 320
Db 901 AGTATTAAGTCATAGTAGAACAGAGATGAACAGAACTCAGATTTTGTGACATCAAGAA 960
```



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Qy 101 PheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThr 120
Db 301 TTCGGGCCACTCTCCCTCAATGACACGTGGCAACTATACCTGTCATGTTAAGGAAACACTACA 360
Qy 121 TyrCysSerLysValAlaPheProLeuGluValValGlnLysAspSerCysPheAsnSer 140
Db 361 TATTGCGAGCAAGTTGCATTTCCCTTGGAGTTGTTCCAAAAGACAGCTGTTTCAATTCC 420
Qy 141 ProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArgIleThrCys 160
Db 421 CCCATGAACTCCCGAGTCATATACTGTATATAGATATATGCAATGCGCATTCAGAGATCACATTGT 480
Qy 161 ProAsnValAspGlyTyrPheProSerSerValLysProThrIleThrTyrMetGly 180
Db 481 CCAATGTAGATGATATTTTCCTTCCAGTGTCAACCCGACTATCATCTTGGTATATATGGGC 540
Qy 181 CysTyrLysIleGlnAsnAsnValIleProGluGlyMetAsnLeuSerPheLeu 200
Db 541 TGTATATAATACAGAAATTTAATAATGTAATACCCGAGGTATGAATCTTGAATTTCTC 600
Qy 201 IleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValThrTyrProGluAsnGly 220
Db 601 ATTGCCTTAATTTCAAAATAATGGAATTTACACATGTGTGTGTATATCCAGAAAAATGGA 660
Qy 221 ArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProLysAsnAla 240
Db 661 CGTACGTTTCACTCACCAGGACTCTGACTGTAAGGTAGTAGGCTCTCCAAAAAATGCA 720
Qy 241 ValProProValIleHisSerProAsnAspHisValValTyrGluLysGluProGlyGlu 260
Db 721 GTGCCCCCTGTGATCCATTACCTAATGATCATGTGTCTATGAGAAAGAACACAGAGAG 780
Qy 261 GluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAspSerArgAsnGluVal 280
Db 781 GAGTACTCATCTCCCTGTACGGTCTAATTTAGTTTCTGATGGATTCCTGCAATGAGGTT 840
Qy 281 TrpTrpThrIleAspGlyLysLysProAspAspIleThrIleAspValThrIleAsnGlu 300
Db 841 TGGTGGACCACTTGATGAAAAAACCCTGATGACATCACTATTGATGTCACCATTAACGAA 900
Qy 301 SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLysLys 320
Db 901 AGTATAAGTCATAGTAAACAGAGATGAACAAGAACTCAGATTTTGACATCAAGAAA 960
Qy 321 ValThrSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAlaLysGlyGlu 340
Db 961 GTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTCTCATGTAGAAGTGCCTCAAGGCGAA 1020
Qy 341 ValAlaLysAlaAlaLysValLysGlnLysValProAlaProArgTyrThrValGlu 359
Db 1021 GTTGCCAAAGCAGCAAGGTGAAGCAGAAAAAGTGCAGCTCCAAAGATACACAGTGGAA 1077
```

RESULT 5

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US-11-144-987-11
; Sequence 11, Application US/111144987
; Publication No. US20050272655A1
; GENERAL INFORMATION:
; APPLICANT: Mellis, Scott
; APPLICANT: Karow, Margaret
; APPLICANT: Yancopoulos, George
; APPLICANT: Papadopoulos, Joanne
; TITLE OF INVENTION: Methods of Using IL-1 Antagonists to Treat Autoinflammatory Disease
; FILE REFERENCE: REG 2090A
; CURRENT APPLICATION NUMBER: US/11/144,987
; PRIOR FILING DATE: 2005-06-03
; PRIOR FILING DATE: 60/577,023
; PRIOR FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 2709
; TYPE: DNA
; ORGANISM: Homo sapiens
```

US-11-144-987-11

```
Alignment Scores:
Pred. No.: 6.08e-184 Length: 2709
Score: 1935.00 Matches: 358
Percent Similarity: 99.72% Conservative: 0
Best Local Similarity: 99.72% Mismatches: 1
Query Match: 52.74% Indels: 0
DB: 7 Gaps: 0
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US-10-061-727-2 (1-687) x US-11-144-987-11 (1-2709)

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Qy 1 MetThrLeuLeuTyrPheValValSerLeuTyrPheTyrGlyIleLeuGlnSerAspAla 20
Db 1 ATCGTGCTTCTGTGGTGTGTAGTGAGTCTCTACTTTTATGGAATCTCTGCAAGATGATGCC 60
Qy 21 SerGluArgCysAspAspTyrGlyLeuAspThrMetArgGlnIleGlnValPheGluAsp 40
Db 61 TCAGAACGCTGCCATGACTGGGACTAGACACCATGAGGCAATCCAAAGTGTTTGAAGAT 120
Qy 41 GluProAlaArgIleLysCysProLeuPheGluHisPheLeuLysPheAsnTyrSerThr 60
Db 121 GAGCCAGCTCGCATCAAGTGCACACTCTTTGAAACACTTCTTGAATTTCAACTACAGACA 180
Qy 61 AlaHisSerAlaGlyLeuThrLeuIleTyrTyrThrArgGlnAspArgAspLeuGlu 80
Db 181 GCCCATTCAGCTGGCTTACTCTGATCTGGTATTTGGACTAGGCGAGGACCGGACCTTTGAG 240
Qy 81 GluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTyr 100
Db 241 GAGCCAAATTAACCTTCGCTCCCGAGAACCGCATTTAGTAGAGAGAAAGATGTCTGTGG 300
Qy 101 PheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThr 120
Db 301 TTCGGGCCCACTCTCTCTCAATGACACTGGCAACTATACCTGTCATGTTAAGGAAACACTACA 360
Qy 121 TyrCysSerLysValAlaPheProLeuGluValValGlnLysAspSerCysPheAsnSer 140
Db 361 TATTGCGCAAGCTTGCATTTCCCTTGGAGTTGTTCCAAAAGACAGCTGTTTCAATTCC 420
Qy 141 ProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArgIleThrCys 160
Db 421 CCATGAAACTCCCGAGTGCATATACTGATATAGAAATATGGCATTCAGAGATCACATTGT 480
Qy 161 ProAsnValAspGlyTyrPheProSerSerValLysProThrIleThrTyrMetGly 180
Db 481 CCAATGTAGATGATATTTTCCTTCCAGTGTCAACCCGACTATCACTTGGTATATGGGC 540
Qy 181 CysTyrLysIleGlnAsnPheAsnValIleProGluGlyMetAsnLeuSerPheLeu 200
Db 541 TGTATATAATACAGAAATTTAATAATGTAATACCCGAGGTATGAATCTTGAATTTCTC 600
Qy 201 IleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValThrTyrProGluAsnGly 220
Db 601 ATTGCCTTAATTTCAAAATAATGGAATTTACACATGTGTGTGTATATCCAGAAAAATGGA 660
Qy 221 ArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProLysAsnAla 240
Db 661 CGTACGTTTCACTCACCAGGACTCTGACTGTAAGGTAGTAGGCTCTCCAAAAAATGCA 720
Qy 241 ValProProValIleHisSerProAsnAspHisValValTyrGluLysGluProGlyGlu 260
Db 721 GTGCCCCCTGTGATCCATTACCTAATGATCATGTGTCTATGAGAAAGAACACAGAGAG 780
Qy 261 GluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAspSerArgAsnGluVal 280
Db 781 GAGTACTCATCTCCCTGTACGGTCTAATTTAGTTTCTGATGGATTCCTGCAATGAGGTT 840
Qy 281 TrpTrpThrIleAspGlyLysLysProAspAspIleThrIleAspValThrIleAsnGlu 300
Db 841 TGGTGGACCACTTGATGAAAAAACCCTGATGACATCACTATTGATGTCACCATTAACGAA 900
Qy 301 SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLysLys 320
```

```
Db 901 AGTATAAGTCATAGTAGAACAGAGTGAACAGAACTCAGATTTTGAGCATCAAGAAA 960
Qy 321 ValThrSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAlaLysGlyGlu 340
Db 961 GTTACCTCTGAGGATCTCAAGCGCAGCTATGCTGTCTAGTAGAAGTGCCAAAGGCCAA 1020
Qy 341 ValAlaLysAlaAlaLysValLysGlnLysValProAlaProArgTyrThrValGlu 359
Db 1021 GTTGCCAAAGCAGCCAGAGGTGAAGCAGAAAAGTGCCAGCTCCCAAGATACACAGTGGAA 1077

RESULT 6
US-11-144-987-13
; Sequence 13, Application US/11144987
; Publication No. US20050272655A1
; GENERAL INFORMATION:
; APPLICANT: Mellis, Scott
; APPLICANT: Karow, Margaret
; APPLICANT: Yancopoulos, George
; APPLICANT: Papadopoulos, Joanne
; FILE OF INVENTION: Methods of Using IL-1 Antagonists to Treat Autoinflammatory Disease
; CURRENT APPLICATION NUMBER: US/11/144,987
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: 60/577,023
; PRIOR FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 2709
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-144-987-13

Alignment Scores:
Pred. No.: 6,08e-184 Length: 2709
Score: 1935.00 Matches: 358
Percent Similarity: 99.72% Conservative: 0
Best Local Similarity: 99.72% Mismatches: 1
Query Match: 52.74% Indels: 0
DB: 7 Gaps: 0

US-10-061-727-2 (1-687) x US-11-144-987-13 (1-2709)
Qy 1 MetThrLeuLeuTrpCysValValSerLeuTyrPheTyrGlyIleLeuGlnSerAspAla 20
Db 1 ATGGTGCTTCGTGTGTGTAGTAGTCTCTACTTTTATGGAATCCTGCAAGTGATGCC 60
Qy 21 SerGluArgCysAspTrpGlyLeuAspThrMetArgGlnIleGlnValPheGluAsp 40
Db 61 TCAGAACGCTGCGATGACTGGGGACTAGACACCATGAGGCAAAATCCAAGTGTGTTGAAGAT 120
Qy 41 GluProAlaArgIleLysCysProLeuPheGluHisPheLeuLysPheAsnTyrSerThr 60
Db 121 GAGCCAGCTCGCATCAAGTGCCCACTCTTTGAACACTCTTTGAACACTCTTTGAACACTAGACACA 180
Qy 61 AlaHisSerAlaGlyLeuThrLeuIleTrpTyrThrArgGlnAspArgAspLeuGlu 80
Db 181 GCCCAATTCAGCTGGCCCTTACTCTGATCTGGTATTGACTAGCAGGACCGGACCTTGAG 240
Qy 81 GluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTrp 100
Db 241 GAGCCAAATTAATCTCCGCTCCCGAGAACCGCATTAAGGAGAAAGATGCTGTGG 300
Qy 101 PheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThr 120
Db 301 TTCCGGCCCACTCTCCTCAATGACACTGGCAACTATACCTGCATCTGATTTAAGGAACACTACA 360
Qy 121 TyrCysSerLysValAlaPheProLeuGluValGlnLysValGlnLysAspSerCysPheAsnSer 140
Db 361 TATTGCAGCAAGTTGCATTTCCCTTGGAAAGTTGTTCAAAAAGACAGCTGTTCAATTTCC 420
Qy 141 ProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArgIleThrCys 160
```

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Db 421 CCCATGAACCTCCAGTGTCATAAACTGTATATAGATATGTCATTCAGAGCATCACTTGT 480
Qy 161 ProAsnValAspGlyTyrPheProSerSerValLysProThrIleThrTyrTrpMetGly 180
Db 481 CCAATGTAGATGATATTTTCCCTTCCAGTGTCAAAACCGACTATACACTTGTGTATATGGGC 540
Qy 181 CysTyrLysIleGlnAsnPheAsnValIleProGluGlyMetAsnLeuSerPheLeu 200
Db 541 TGTATATAAATACAGAAATTTTAATAATGTAATACCCGNAAGGTATGNACTTGAGTTTCCTC 600
Qy 201 IleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValThrTyrProGluAsnGly 220
Db 601 ATTGCCTTAATTTCAAAATAATGGAATTTACACATGTGTGTGTATACATATCCAGAAAATGGA 660
Qy 221 ArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProLysAsnAla 240
Db 661 CGTACGTTTTCATCTCACCAGGACTCTGACTGTAAGGTAGTAGGCTCTCCAAAAAATGCA 720
Qy 241 ValProProValIleHisSerProAsnAspHisValValTyrGluLysGluProGlyGlu 260
Db 721 GTGCCCCCTGTGATCCATTACCTAATGATCATGTGTCTATGAGAAAGAACCCAGGAGAG 780
Qy 261 GluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAspSerArgAsnGluVal 280
Db 781 GAGCTACTCATTCCTGTACGGTCTATTTTATGTTTCTGTATGATGATTCGCAATGAGGTT 840
Qy 281 TrpTrpThrIleAspGlyLysLysProAspAspIleThrIleAspValThrIleAsnGlu 300
Db 841 TGGTGGACCATTTGATGAAAAAAACCTGATGACATCACTATTGATGTCCACATTAAACGAA 900
Qy 301 SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLysLys 320
Db 901 AGTATAGTCATAGTAAGACAGAGATGAAACAGAACTCAGATTTTGAGCATCAAGAAA 960
Qy 321 ValThrSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAlaLysGlyGlu 340
Db 961 GTTACCTCTGAGGATCTCAAGCGCAGCTATGCTGTCTATGCTAGAAAGTGCCAAAGGCCAA 1020
Qy 341 ValAlaLysAlaAlaLysValLysGlnLysValProAlaProArgTyrThrValGlu 359
Db 1021 GTTGCCAAAGCAGCCAGAGGTGAAGCAGAAAAGTGCCAGCTCCCAAGATACACAGTGGAA 1077

RESULT 7
US-11-144-987-1
; Sequence 1, Application US/11144987
; Publication No. US20050272655A1
; GENERAL INFORMATION:
; APPLICANT: Mellis, Scott
; APPLICANT: Karow, Margaret
; APPLICANT: Yancopoulos, George
; APPLICANT: Papadopoulos, Joanne
; FILE OF INVENTION: Methods of Using IL-1 Antagonists to Treat Autoinflammatory Disease
; CURRENT APPLICATION NUMBER: US/11/144,987
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: 60/577,023
; PRIOR FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2733
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-144-987-1

Alignment Scores:
Pred. No.: 1.97e-183 Length: 2733
Score: 1930.00 Matches: 357
Percent Similarity: 99.72% Conservative: 0
Best Local Similarity: 99.72% Mismatches: 1
Query Match: 52.60% Indels: 0
DB: 7 Gaps: 0
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US-10-061-727-2 (1-687) x US-11-144-987-1 (1-2733)

```
Qy 1 MetThrLeuLeuTrpCysValSerLeuTyrPheTyrGlyIleLeuGlnSerAspAla 20
Db 1 ATGGTGCTTCTGTGTGTAGTGAGTCTCTACTATTTATGGAATCCTGCAAGGTGATGCC 60
Qy 21 SerGluArgCysAspAspTrpGlyLeuAspThrMetArgGlnIleGlnValPheGluAsp 40
Db 61 TCAGAAACGCTCGCATGACTGGGGACTAGACACCATGAGGCAAAATCCCAAGTGTTTGAAGAT 120
Qy 41 GluProAlaArgIleLysCysProLeuPheGluHisPheLeuLysPheAsnTyrSerThr 60
Db 121 GAGCAGACTCGCATCAAGTGGCCCACTCTTTGAACACTCTTTGAAATTCACACTACAGACA 180
Qy 61 AlaHisSerAlaGlyLeuThrLeuIleTrpTyrTrpArgGlnAspArgAspLeuGlu 80
Db 181 GCCCATTTACGCTGCCCTTACTCTGATCTGGTATTGGACTAGGCAGGACCGGACCTTTGAG 240
Qy 81 GluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTrp 100
Db 241 GAGCCAAATTAACCTTCCGCCCTCCCGAGAACCGCATTAGTAAGGAGAAAGATGTCTGTGG 300
Qy 101 PheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThr 120
Db 301 TTCCGGCCCACTCTCCATAGACACTGGCACTATACCTGCATGTTAAGGAACACTACA 360
Qy 121 TyrCysSerLysValAlaPheProLeuGluValValGlnLysAspSerCysPheAsnSer 140
Db 361 TATTGCAGCAAGTTGCATTTCCCTTGGAAAGTTGTTCAAAAAGACACGCTGTTCAATTC 420
Qy 141 ProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArgIleThrCys 160
Db 421 CCCATGAACATCCAGTGGCAATAACTGTATATAGAATATGGCATTCAGAGGATCACTTGT 480
Qy 161 ProAsnValAspGlyTyrPheProSerSerValLysProThrIleThrTrpTyrMetGly 180
Db 481 CCAATGTAGATGATATTTTCTTCCAGTGTCCAAACCGACTATCACTTGTATATATGGGC 540
Qy 181 CysTyrLysIleGlnAsnPheAsnValIleProGluGlyMetAsnLeuSerPheLeu 200
Db 541 TGTATATAAATACAGAAATTTAATAATGTAATACCCGAGGATGAACCTTGAGTTTCCCTC 600
Qy 201 IleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValThrTyrProGluAsnGly 220
Db 601 ATTGCCCTTAATTTCAAATAATAGGAATTTACACATGTGTGTTTACATATCCAGAAAAATGGA 660
Qy 221 ArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProLysAsnAla 240
Db 661 CGTACGTTTCATCTCACAGGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAAAATGCA 720
Qy 241 ValProProValIleHisSerProAsnAspHisValValTyrGluLysGluProGlyGlu 260
Db 721 GTGCCCCCTGTGATCCATTACCTAATGATCATGTGTGCTATGAGAAAGAACCCAGGAGAG 780
Qy 261 GluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAspSerArgAsnGluVal 280
Db 781 GAGCTACTCAATCCCTGTACGGTCTATTTTGTAGTTTCTGATGGATTCCTCGCAATGAGGTT 840
Qy 281 TrpTrpThrIleAspGlyLysLysProAspAspIleThrIleAspValThrIleAsnGlu 300
Db 841 TGTGGNCCATTGATGGAAAAAACCCTGATGACATCACTATTGATGTACCATTAACGAA 900
Qy 301 SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLysLys 320
Db 901 AGTATAAGTCATAGTAGAACAGAAAGATGAACAAGAACTCAGATTTTGGACATCAAGAAA 960
Qy 321 ValThrSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAlaLysGlyGlu 340
Db 961 GTTACTCTCTGAGGATCTCAAGCCGACGCTATGCTCTGTCATGCTAGAAAGTGCAGAAAGCGAA 1020
Qy 341 ValAlaLysAlaAlaLysValLysGlnLysValProAlaProArgTyrThrVal 358
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Db 1021 GTTGCCAAACGACGCAAGGTGAAGCAGAAAAAGTGCCAGCTCCAAGATACACAGTG 1074

RESULT 8

US-11-144-987-3

; Sequence 3, Application US/11144987

; Publication No. US20050272655A1

; GENERAL INFORMATION:

; APPLICANT: Mellis, Scott

; APPLICANT: Karow, Margaret

; APPLICANT: Yancopoulos, George

; APPLICANT: Papadopoulos, Joanne

; TITLE OF INVENTION: Methods of Using IL-1 Antagonists to Treat Autoinflammatory Disease

; FILE REFERENCE: REG 2090A

; CURRENT APPLICATION NUMBER: US/11/144,987

; CURRENT FILING DATE: 2005-06-03

; PRIOR FILING DATE: 2004-06-04

; NUMBER OF SEQ ID NOS: 26

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 3

; LENGTH: 2703

; TYPE: DNA

; ORGANISM: Homo sapiens

US-11-144-987-3

Alignment Scores:

Pred. No.:	1,15e-173	Length:	2703
Score:	1833.00	Matches:	339
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	49.96%	Indels:	0
DB:	7	Gaps:	0

US-10-061-727-2 (1-687) x US-11-144-987-3 (1-2703)

Qy 21 SerGluArgCysAspAspTrpGlyLeuAspThrMetArgGlnIleGlnValPheGluAsp 40

Db 997 TCAGAACGCTGGCATGACTGACCTGGGACTAGACACCATGAGGCAAAATCCCAAGTGTTTGAAGAT 1056

Qy 41 GluProAlaArgIleLysCysProLeuPheGluHisPheLeuLysPheAsnTyrSerThr 60

Db 1057 GAGCCAGCTCGCATCAAGTGCCCACTCTTTGAACACTCTCTTGAATTCACACTACAGACA 1116

Qy 61 AlaHisSerAlaGlyLeuThrLeuIleTrpTyrTrpThrArgGlnAspArgAspLeuGlu 80

Db 1117 GCCCATTCAGCTGCCCTTACTCTGATCTGCTATTTGGACTAGGCAGGACCGGACCTTTGAG 1176

Qy 81 GluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTrp 100

Db 1177 GAGCCAAATTAACCTTCCGCTTCCCGAGAACCCGCAATTAGTAAGGAGAAAGATGTGCTGTGG 1236

Qy 101 PheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThr 120

Db 1237 TTCCGGCCCCACTCTCTCAATGACACTGGCACTATACCTGTCATGTTAAGGAACACTACA 1296

Qy 121 TyrCysSerLysValAlaPheProLeuGluValValGlnLysAspSerCysPheAsnSer 140

Db 1297 TATTGAGCAAAAGTTGCAATTCCTTTGGAAGTTGTTCAAAAAGACAGCTGTTTCAATTCC 1356

Qy 141 ProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArgIleThrCys 160

Db 1357 CCCATGAACCTCCAGTGCATAACTGTATATAGAATATGGCAATCAGAGGATCACTTGT 1416

Qy 161 ProAsnValAspGlyTyrPheProSerSerValLysProThrIleThrTrpTyrMetGly 180

Db 1417 CCBAATGTAGATGGATATTTTCTTCCAGTGTCAAAACCGACATCACTTGGTATATGGGC 1476

Qy 181 CysTyrLysIleGlnAsnPheAsnAsnValIleProGluGlyMetAsnLeuSerPheLeu 200

Db 1477 TGTATATAAATAACAGAAATTTAATAATGTAATACCCGAAAGGTATGAACCTTGAAGTTCCTC 1536

Qy 201 IleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValThrTyrProGluAsnGly 220

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Db 1537 ATTGCCTTAATTTCAAATAATGGAATATACACATGTTGTTTACATATCCAGAAAATGGA 1596
Qy 221 ArgThrPheHisLeuThrArgThrLeuThrVallysValValGlySerProLysAsnAla 240
Db 1597 CGTAGCTTTCATCTCACCGAGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAATAATGCA 1656
Qy 241 ValProProValIleHisSerProAsnAspHisValValTyrGluLysGluProGlyGlu 260
Db 1657 GTGCCCTCTGTGATCCATTCACCTAATGATCATGTGGTCTATGAGAAAGAACCCAGGAG 1716
Qy 261 GluLeuLeuLeuProCysThrValTyrPheSerPheLeuMetAspArgAsnGluVal 280
Db 1717 GAGCTACTCATTTCCCTGTACGGCTATTTTATGTTTCTGATGGATTCGCAATGAGGTT 1776
Qy 281 TrpTrpThrIleAspGlyLysLysProAspAspIleThrIleAspValThrIleAsnGlu 300
Db 1777 TGGTGGACCATTTGATGGAAAAAACCCTGATGACATCACTATTGATGTCACCATTAACGAA 1836
Qy 301 SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLysLys 320
Db 1837 AGTATAAGTCATAGTAGAACAGAGATGAACAAGAACTCAGATTTTGAGCATCAAGAAA 1896
Qy 321 ValThrSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAlaLysGlyGlu 340
Db 1897 GTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTCATGCTAGAGATGCCAAAGCGGAA 1956
Qy 341 ValAlaLysAlaAlaLysValLysGlnLysValProAlaProArgTyrThrValGlu 359
Db 1957 GTTGCAAAGCGCCAGGTGAGCAGAAAGTGCCAGCTCCAAAGATACACAGTGGAA 2013

RESULT 9
US-11-144-987-5
; Sequence 5, Application US/11144987
; Publication No. US20050272655A1
; GENERAL INFORMATION:
; APPLICANT: Mellis, Scott
; APPLICANT: Karow, Margaret
; APPLICANT: Yancopoulos, George
; APPLICANT: Papadopoulos, Joanne
; TITLE OF INVENTION: Methods of Using IL-1 Antagonists to Treat Autoinflammatory Disease
; CURRENT APPLICATION NUMBER: US/11/144,987
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: 60/577,023
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-144-987-5

Alignment Scores:
Pred. No.: 1,15e-173 Length: 2709
Score: 1833.00 Matches: 339
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 49.96% Indels: 0
DB: 7 Gaps: 0

US-10-061-727-2 (1-687) x US-11-144-987-5 (1-2709)

Qy 21 SerGluArgCysAspAspTrpGlyLeuAspThrMetArgGlnIleGlnValPheGluAsp 40
Db 987 TCAGAACCTCGCATGATCGGGACTAGACACCATGAGGCAATCCAAAGTCTTTGAAGAT 1056
Qy 41 GluProAlaArgIleLysCysProLeuPheGluHisPheLeuLysPheAsnTyrSerThr 60
Db 1057 GAGCCAGCTCGCATCAAGTGGCCACTCTTTGAACACTCTTTGAATTCACATACAGCACA 1116
Qy 61 AlaHisSerAlaGlyLeuThrLeuIleTrpTyrTrpThrArgGlnAspArgAspLeuGlu 80
Db 1116 GAGCCAGCTCGCATCAAGTGGCCACTCTTTGAACACTCTTTGAATTCACATACAGCACA 1116
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Db 1117 GCCCATTCAGCTGGCCTTACTCTGATCTGGTATTGGACATAGCAGGACCGGACCTTGAG 1176
Qy 81 GluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTrp 100
Db 1177 GAGCCAAATTAATTTCCGCTCTCCCGAGAACCGCATTTAGTAGGAGAAAGATGTGTGTGG 1236
Qy 101 PheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThr 120
Db 1237 TTCCGGCCCACTCTCTCAATGACATGCGCAACTATACCTGTCATGTTAAGGAACACTACA 1296
Qy 121 TyrCysSerLysValAlaPheProLeuGluValValGlnLysAspSerCysPheAsnSer 140
Db 1297 TATTGCAAGAAAGTTGCATTTCCCTTGAAGTGTTCAAAAAGACAGCTGTTTCAATTC 1356
Qy 141 ProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArgIleThrCys 160
Db 1357 CCCATGAACCTCCAGTGCATAAACTGTATATAGNATATGGCATTCAGAGNATCACTGT 1416
Qy 161 ProAsnValAspGlyTyrPheProSerSerValLysProThrIleThrTrpTyrMetGly 180
Db 1417 CCAATGTAGATGATATTTTCCCTCCAGTGTCAAAACCGCATATCACCTGGTATATGGGC 1476
Qy 181 CysTyrLysIleGlnAsnPheAsnAsnValIleProGluGlyMetAsnLeuSerPheLeu 200
Db 1477 TGTATATAAATACAGAAATTTTAAATATGTAATACCCGAAGGTATGAACCTTGAGTTT 1536
Qy 201 IleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValThrTyrProGluAsnGly 220
Db 1537 ATTGCCTTAATTTCAAATTAATGGAATTTACACATGTGTTGTACATATCCAGAAAATGGA 1596
Qy 221 ArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProLysAsnAla 240
Db 1597 CGTAGCTTTCATCTCACCGAGACTCTGACTCTAAAGGTAGTAGGCTCTCCAAAATAATGCA 1656
Qy 241 ValProProValIleHisSerProAsnAspHisValValTyrGluLysGluProGlyGlu 260
Db 1657 GTGCCCTCTGTGATCCATTTCACTCAATGATCATGTGGTCTATGAGAAAGAACCCAGGAG 1716
Qy 261 GluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAspArgAsnGluVal 280
Db 1717 GAGCTACTCATTTCCCTGTACGGCTATTTTATGTTTCTGATGGATTCGCAATGAGGTT 1776
Qy 281 TrpTrpThrIleAspGlyLysLysProAspAspIleThrIleAspValThrIleAsnGlu 300
Db 1777 TGGTGGACCATTTGATGGAAAAAACCCTGATGACATCACTATTGATGTCAACCATTAACGAA 1836
Qy 301 SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLysLys 320
Db 1837 AGTATAAGTCATAGTAGAACAGAGATGAACAAGAACTCAGATTTTTCAGCATCAAGAAA 1896
Qy 321 ValThrSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAlaLysGlyGlu 340
Db 1897 GTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTCATGCTAGAGTGGCCAAAGCGGAA 1956

RESULT 10
US-11-144-987-7
; Sequence 7, Application US/11144987
; Publication No. US20050272655A1
; GENERAL INFORMATION:
; APPLICANT: Mellis, Scott
; APPLICANT: Karow, Margaret
; APPLICANT: Yancopoulos, George
; APPLICANT: Papadopoulos, Joanne
; TITLE OF INVENTION: Methods of Using IL-1 Antagonists to Treat Autoinflammatory Disease
; CURRENT APPLICATION NUMBER: US/11/144,987
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: 60/577,023
; PRIOR FILING DATE: 2004-06-04
```

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; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 2709
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-144-987-7

Alignment Scores:
Pred. No.: 1,15e-173 Length: 2709
Score: 1833.00 Matches: 339
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 49.96% Indels: 0
DB: 7 Gaps: 0

US-10-061-727-2 (1-687) x US-11-144-987-7 (1-2709)

Qy 21 SerGluArgCysAspAspTrpGlyLeuAspThrMetArgGlnIleGlnValPheGluAsp 40
Db 997 TCAGAACGCTCGAGTACTGGGGACTAGACACCAATGAGGCAAAATCCAAAGTGTGTTGAAGAT 1056

Qy 41 GluProAlaArgIleLysCysProLeuPheGluHisPheLeuLysPheAsnTyrSerThr 60
Db 1057 GAGCCAGCTCGCATCAAGTGCCTCTTTGAACACTTCTTGAATTCACACTACAGCACA 1116

Qy 61 AlahisSerAlaGlyLeuThrLeuIleTrpTyrThrArgGlnAspArgAspLeuGlu 80
Db 1117 GCCCATTTTCAGTGGCCTTACTCTGATCTGGTATTGGACTAGGCAGGACCGGACCTTTGAG 1176

Qy 81 GluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTrp 100
Db 1177 GAGCCAATTAATCTCCGCTCCCGAGAACCGCATTAAGAGGAAAGATGTGCTGTGG 1236

Qy 101 PheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThr 120
Db 1237 TTCGGGCCACTCTCCTCAATGACACTGGCACTATACCTGCATGTTAAGGAACACTACA 1296

Qy 121 TyrCysSerLysValAlaPheProLeuGluValValGlnLysAspSerCysPheAsnSer 140
Db 1297 TATTGCGAGCAAGTTGCATTTCCCTTGGAACTGTTCAAAAAGACAGCTGTTCAATTC 1356

Qy 141 ProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArgIleThrCys 160
Db 1357 CCCATGAACATCCCGATGCGATAAACTGTATAGAAATATGGCAATTCAGAGATCACTGT 1416

Qy 161 ProAsnValAspGlyTyrPheProSerSerValLysProThrIleThrTyrTrpMetGly 180
Db 1417 CCAATGTAGATGGATATTTCTTCCAGTGTCAACCGGACTATCACTTGGTATATGGGC 1476

Qy 181 CysTyrLysIleGlnAsnPheAsnAsnValIleProGluGlyMetAsnLeuSerPheLeu 200
Db 1477 TGTATATAAATACAGAAATTTAATAATGTAATACCCGAAGGTATGAATTTGAGTTTCCTC 1536

Qy 201 IleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValThrTyrProGluAsnGly 220
Db 1537 ATTGCCCTTAATTTCAAAATAATGGAATTTACACATGTGTTGTATACATATCCAGAAAAATGGA 1596

Qy 221 ArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProLysAsnAla 240
Db 1597 CGTAGCTTTCATCTCACCAGGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAAAATGCA 1656

Qy 241 ValProProValIleHisSerProAsnAspHisValValTyrGluLysGluProGlyGlu 260
Db 1657 GTGCCCCCTGTGATCCATTACCTTAATGATCATGTGCTGTATGAGAAAGAACCCAGGAGAG 1716

Qy 261 GluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAspSerArgAsnGluVal 280
Db 1717 GAGTACTCAATTCCTGTGACGGTCTATTTAGTTTTCCTGATGAGATTCCTCGCAATGAGGTT 1776

Qy 281 TrpTrpThrIleAspGlyLysLysProAspAspIleThrIleAspValThrIleAsnGlu 300
Db 1777 TGGTGGACCATTTGATGGAAAAAACCCTGATGACATCACTATTGATGTACCATTTACGAA 1836
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Qy 301 SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLysLys 320
Db 1837 AGTATAAGTTCATAGTACAGACAGAAAGATGAAACAAGAACTCAGATTTTTCAGCATCAAGAAA 1896

Qy 321 ValThrSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAlaLysGlyGlu 340
Db 1897 GTTACCTCTCAGGATCTCAAGCCGACGCTATGTCTCATGTAGAAAGTGCACAAAGGGCGAA 1956

Qy 341 ValAlaLysAlaAlaLysValLysGlnLysValProAlaProAspGlyThrValGlu 359
Db 1957 GTTGCCTCAAGACGCAAGGTGAAGCAGAAAGTGCCAGCTCCAGATACACAGTGGAA 2013

RESULT 11
US-11-144-987-17
; Sequence 17, Application US/11144987
; Publication No. US20050272655A1
; GENERAL INFORMATION:
; APPLICANT: Mellis, Scott
; APPLICANT: Karow, Margaret
; APPLICANT: Yancopoulos, George
; APPLICANT: Papadopoulos, Joanne
; TITLE OF INVENTION: Methods of Using IL-1 Antagonists to Treat Autoinflammatory Disease
; FILE REFERENCE: REG 2090A
; CURRENT APPLICATION NUMBER: US/11/144,987
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: 60/577,023
; PRIOR FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 2754
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-144-987-17

Alignment Scores:
Pred. No.: 2,37e-173 Length: 2754
Score: 1830.00 Matches: 340
Percent Similarity: 97.99% Conservative: 1
Best Local Similarity: 97.70% Mismatches: 7
Query Match: 49.88% Indels: 0
DB: 7 Gaps: 0

US-10-061-727-2 (1-687) x US-11-144-987-17 (1-2754)

Qy 18 SerAspAlaSerGluArgCysAspAspTrpGlyLeuAspThrMetArgGlnIleGlnVal 37
Db 1036 TCACAGTTCACAGACGCTGCGATGACTGGGGACTAGACACCATGAGGCAAAATCCAAAGTG 1095

Qy 38 PheGluAspGluProAlaArgIleLysCysProLeuPheGluHisPheLeuLysPheAsn 57
Db 1096 TTTGAAGATGAGCAGCTGCGATCAAGTGCCTCTTTGAACACTTCTTTGAAATTCAC 1155

Qy 58 TyrSerThrAlaHisSerAlaGlyLeuThrLeuIleTrpTyrThrArgGlnAspArg 77
Db 1156 TACAGACACAGCCCATTTTCAGCTGGCCTTACTCTGATCTGGTATTGGACTAGGACGACCGG 1215

Qy 78 AspLeuGluGluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAsp 97
Db 1216 GACCTTGAGGAGGCAATTAATCTTCCGCTCCCGAGAACCGCATTTAGTAGGAGAAAGAT 1275

Qy 98 ValLeuTrpPheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArg 117
Db 1276 GTGCTGTGGTTCGGGCCCACTCTCTCAATGACACTGGCAACTATACCTCATCTCATGTTAAAGG 1335

Qy 118 AsnThrThrTyrCysSerLysValAlaPheProLeuGluValValGlnLysAspSerCys 137
Db 1336 AACACTACATATATTCAGCAGCAAGTTGCATTTCCCTTGGAAAGTGTTCCTTCAAAAAGACAGCTGT 1395

Qy 138 PheAsnSerProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArg 157
Db 1396 TTCATTTCCCCCATGAAACTCCCGATGCAATAAATCTGTATATAGATATGCGCATTCAGAGG 1455
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QY 158 ileThrCysProAsnValAspGlyTyrPheProSerSerVallyProThrIleThrTrp 177
Db 1456 ATCACTGTGCCAAATGTAGATGATATTTCTTCCAGTGTCACACCGACTATCACTTGG 1515
QY 178 TyrMetGlyCysTyrIlyIleGlnAsnPheAsnAsnValIleProGluGlyMetAsnLeu 197
Db 1516 TATATGGGCTGTATATAAATACAGAAATTTTAATAATGTAAATACCCGAAAGGTATGAACITG 1575
QY 198 SerPheLeuIleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValThrTyrPro 217
Db 1576 AGTTTCTCTATGCTTAAATTTCAATAATGGAATTTACACATGTGTTGTATACATATCCA 1635
QY 218 GluAsnGlyArgThrPheHisLeuThrArgThrLeuThrValIlyValIlyValGlySerPro 237
Db 1636 GAAATATGGACGTACGTTTCATCTCACCAGGACTCTGACTGTAAAGGTAGTAGGCTCTCCA 1695
QY 238 LysAsnAlaValProProValIleHisSerProAsnAspHisValValTyrGluIlyGlu 257
Db 1696 AAAAATGCGAGTGCCTCTGTATCCATTCACTTAATGATGATGATGATGATGATGATGATG 1755
QY 258 ProGlyGluGluLeuLeuLeuProCysThrValTyrPheSerPheLeuMetAspSerArg 277
Db 1756 CCAGGAGAGAGCTACTCAATCCCTGTACGGTCTATTTTAGTGTCTTCTGATGGATTTCTCGC 1815
QY 278 AsnGluValTrpTrpThrIleAspGlyIlyLysLysProAspAspIleThrIleAspValThr 297
Db 1816 AATGAGTGTGCTGGACCATTCATGGAATAAATCACTGATGATGATGATGATGATGATGATG 1875
QY 298 IleAsnGluSerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSer 317
Db 1876 ATTAACGAAAGTATAAGTCATAGTAGAACAGAAAGTAAAGAACTCAGATTTTGAGC 1935
QY 318 IleLysLysValThrSerGluAspLeuLysLysValIlyValIlyValProAlaProArgTyrThr 357
Db 1936 ATCAAGAAGTTTACCTCTGAGGATCTCAAGCGCAGCTATGCTGTCATGCTAGAAAGTCC 1995
QY 358 ValGluLeuAlaCysGlyPheGly 365
Db 2056 GGTCCGGAGAGTCCAAATACGGT 2079

RESULT 12
US-11-144-987-19
; Sequence 19, Application US/11144987
; Publication No. US20050272655A1
; GENERAL INFORMATION:
; APPLICANT: Karow, Margaret
; APPLICANT: Mellis, Scott
; APPLICANT: Yancopoulos, George
; APPLICANT: Papadopoulos, Joanne
; TITLE OF INVENTION: Methods of Using IL-1 Antagonists to Treat Autoinflammatory Disease
; FILE REFERENCE: REG 2090A
; CURRENT APPLICATION NUMBER: US/11/144,987
; PRIORITY FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: 60/577,023
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 2754
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-144-987-19

Alignment Scores:
Pred. No.: 2,378-173 Length: 2754
Score: 1830.00 Matches: 340
Percent Similarity: 97.99% Conservative: 1
Best Local Similarity: 97.70% Mismatches: 7
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```
Query Match: 49.88% Indels: 0
DB: 7 Gaps: 0
US-10-061-727-2 (1-687) x US-11-144-987-19 (1-2754)
QY 18 SerAspAlaSerGluArgCysAspAspTrpGlyLeuAspThrMetArgGlnIleGlnVal 37
Db 1036 TCCAGCTTCTCAGAACCGTGCATGCTGGGACTAGACACCATCAGGCAATCCAAAGTG 1095
QY 38 PheGluAspGluProAlaArgIleLysCysProLeuPheGluHisPheLeuLysPheAsn 57
Db 1096 TTTGAAGATGAGCCAGCTCGCATCAAGTGCACACTCTTTTGAACACTCTTCTTGAATTTCAAC 1155
QY 58 TyrSerThrAlaHisSerAlaGlyLeuThrLeuIleTrpTyrTrpThrArgGlnAspArg 77
Db 1156 TACAGCAGACCCCATTCAGCTGGCTTACTCTGATCTGCTATTTGGACTAGGACAGCCGG 1215
QY 78 AspLeuGluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAsp 97
Db 1216 GACCTTGAGGAGCCAAATTAACCTTCGCCCTCCCGAGAACCGCATTTAGTAAGGAGAAAGAT 1275
QY 98 ValLeuTrpPheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArg 117
Db 1276 GTGCTGTGGTTCGGGCCCACTCTCTCAATGACACTGGCAACTATACCTGCTGATGTTAAGG 1335
QY 118 AsnThrThrTyrCysSerLysValAlaPheProLeuGluValValGlnLysAspSerCys 137
Db 1336 AACACTACATATTCGCGCAAGTTGCATTTCCCTTGGAAAGTTGTTCAAAAAGACAGCTGT 1395
QY 138 PheAsnSerProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArg 157
Db 1396 TTCAATTTCCCAATGAAACTCCAGTGCATAACTGATATAGAAATATGGCATTCAGAGG 1455
QY 158 IleThrCysProAsnValAspGlyTyrPheProSerSerValLysProThrIleThrTrp 177
Db 1456 ATCACTTGTCCAAATGTAGATGATATTTTCCCTTCCAGTGTCAAACCGCATATCACTTGG 1515
QY 178 TyrMetGlyCysTyrLysIleGlnAsnPheAsnValIleProGluGlyMetAsnLeu 197
Db 1516 TATATGGCTGTTTAAATACAGAAATTTTAATGTATATACCCGAAAGGTATGAACITG 1575
QY 198 SerPheLeuIleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValThrTyrPro 217
Db 1576 AGTTTCTCTCAATGCTTAAATTTCAAAATAATGAAATATACACATGCTGTTGTTTACATATCCA 1635
QY 218 GluAsnGlyArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerPro 237
Db 1636 GAAATATGGACGTACGTTTTCATCTCACCAGGACTCTGACTGTAAAGGTAGTAGGCTCTCCA 1695
QY 238 LysAsnAlaValProProValIleHisSerProAsnAspHisValValTyrGluLysGlu 257
Db 1696 AAAATGCGAGTGCCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1755
QY 258 ProGlyGluGluLeuLeuLeuProCysThrValTyrPheSerPheLeuMetAspSerArg 277
Db 1756 CCAGGAGAGGAGTACTCACTTCCCTGTCAGGCTCTATTTTAGTGTCTTCTGATGGATTTCTCGC 1815
QY 278 AsnGluValTrpTrpThrIleAspGlyLysLysProAspAspIleThrIleAspValThr 297
Db 1816 AATGAGGTTTGGTGGACCAATTTGATGGAAAAAACCTGATGATGATGATGATGATGATGATG 1875
QY 298 IleAsnGluSerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSer 317
Db 1876 ATTAACGAAAGTATAAGTCATAGTAGAACAGAAAGTAAACAGAACTCAGATTTTGAGC 1935
QY 318 IleLysLysValThrSerGluAspLeuLysLysArgSerTyrValCysHisAlaArgSerAla 337
Db 1936 ATCAAGAAGTTTACCTCTGAGGATCTCAAGCGCAGCTATGCTGCTCATGCTAGAAAGTCC 1995
QY 338 LysGlyGluValAlaLysAlaLysValIlyValIlyValProAlaProArgTyrThr 357
Db 1996 AAAGCGAAGTTGCCAAGACGCCAAGGTGAGCAGAAAGTGCCAGCTCCCAAGATACACA 2055
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Qy 358 ValGluLeuAlaCysGlyPheGly 365
Db 2056 GTGTCGGAGAGTCCAAATACGGT 2079

RESULT 13
US-11-144-987-15
; Sequence 15, Application US/11144987
; Publication No. US20050272655A1
; GENERAL INFORMATION:
; APPLICANT: Mellis, Scott
; APPLICANT: Karow, Margaret
; APPLICANT: Yancopoulos, George
; APPLICANT: Papadopoulos, Joanne
; TITLE OF INVENTION: Methods of Using IL-1 Antagonists to Treat Autoinflammatory Disease
; FILE REFERENCE: REG 2090A
; CURRENT APPLICATION NUMBER: US/11/144,987
; PRIOR FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: 60/577,023
; PRIOR FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 2748
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-144-987-15

Alignment Scores:
Pred. No.: 2,98e-173 Length: 2748
Score: 1829.00 Matches: 339
Percent Similarity: 99.41% Conservative: 0
Best Local Similarity: 99.41% Mismatches: 2
Query Match: 49.85% Indels: 0
DB: 7 Gaps: 0

US-10-061-727-2 (1-687) x US-11-144-987-15 (1-2748)

Qy 18 SerAspAlaSerGluAArgCysAspTrpGlyLeuAspThrMetArgGlnIleGlnVal 37
Db 1036 TCCACGTCTTCAGAACCTCGCATGCTGGGACTAGACACCATGAGGCAATCCAAAGTG 1095

Qy 38 PheGluAspGluProAlaArgIleLysCysProLeuPheGluHisPheLeuLysPheAsn 57
Db 1096 TTTGAAGATGACGACGCTCGCATCAAGTCCCACTCTTTGAACACTCTTTGAAATTCAC 1155

Qy 58 TyrSerThrAlaHisSerAlaGlyLeuThrLeuIleTrpTyrTrpThrArgGlnAspArg 77
Db 1156 TACAGCACAGCCCATTCAGCTGGCTTACTCTGATCTGGTATTGGACTAGCAGGACCG 1215

Qy 78 AspleuGluGluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAsp 97
Db 1216 GACCTTGAGGAGCAATTAATCTCCCGCTCCCGAGAACCGCATTAGTAAGGAGAAAGAT 1275

Qy 98 ValLeuTrpPheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArg 117
Db 1276 GTGCTGTGGTTCGGCCCATCTCTCTCAATGACACTGGCACTATACCTCATGTTAAGG 1335

Qy 118 AsnThrThrTyrCysSerLysValAlaPheProLeuGluValValGlnLysAspSerCys 137
Db 1336 AACACTACATATTGCAGCAAGTTGCAATTTCCCTTGGAAAGTTGTTCAAAAAGACAGCTGT 1395

Qy 138 PheAsnSerProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArg 157
Db 1396 TTCAATTTCCCCCAATGAACCTCCAGTGCATAAACTGATATAGAAATATGCGCATTCAGAG 1455

Qy 158 IleThrCysProAsnValAspGlyTyrPheProSerSerValLysProThrIleThrTrp 177
Db 1456 ATCACTGTCCAAATGTAGATGATATTTTCCTTCAGTGTCAACCGCATCATCCTTGG 1515

Qy 178 TyrMetGlyCysTyrIleGlnAsnPheAsnValIleProGluGlyMetAsnLeu 197
Db 1516 TATATGGCTGTTATAAAATACAGAAATTTTAAATATGTAATACCCGAAAGGTATGAACCTTG 1575

Qy 198 SerPheLeuIleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValThrTyrPro 217
Db 1576 AGTTTCTCATTCGCTTAATTTCAAATAATGAAATTTACACATGTTGTTTACATATCCA 1635

Qy 218 GluAsnGlyArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerPro 237
Db 1636 GAAATATGGACGTAGTTTCATCTCACCAGGACTCTGACTGTAAAGGTAGTAGGCTCTCCA 1695

Qy 238 LysAsnAlaValProProValIleHisSerProAsnAspHisValValTyrGluLysGlu 257
Db 1696 AAAATGTCAGTGGCCCTGTGATCCATTACCTAATCATCATGTGGTCTATGAGAAAGAA 1755

Qy 258 ProGlyGluGluLeuLeuProCysThrValTyrPheSerPheLeuMetAspSerArg 277
Db 1756 CCAGGAGAGGAGCTACTCATTCCTGTACGCTCTATTTAGTTTCTGTAGTGGATTCTCGC 1815

Qy 278 AsnGluValTrpTrpThrIleAspGlyLysLeuProAspAspIleThrIleAspValThr 297
Db 1816 AATGAGGTTTGGTGGACCATTTGATGAAAAAACCCTGATGACATCATTTGATGTCAAC 1875

Qy 298 IleAsnGluSerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSer 317
Db 1876 ATTAACGAAAGTATAGTCATAGTACAGACAGAGATGAACAGAACTCAGATTTTCAGC 1935

Qy 318 IleLysLysValThrSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAla 337
Db 1936 ATCAAGAAAGTTACCTCTGAGGATCTCAAGCGCAGCTATGCTGTCATGTAGAAAGTGCC 1995

Qy 338 LysGlyGluValAlaLysAlaLysValLysGlnLysValProAlaProArgTyrThr 357
Db 1996 AAAGGCGAAGTTCCAAAGCAGCAAGGTGAAGCAGAAAGTGCCAGCTCCCAAGATACACA 2055

Qy 358 Val 358
Db 2056 GTG 2058

RESULT 14
US-10-995-561-365
; Sequence 365, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 365
; LENGTH: 2188
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-365

Alignment Scores:
Pred. No.: 5,46e-32 Length: 2188
Score: 425.50 Matches: 152
Percent Similarity: 39.42% Conservative: 92
Best Local Similarity: 24.56% Mismatches: 231
Query Match: 11.60% Indels: 145
DB: 6 Gaps: 22

US-10-061-727-2 (1-687) x US-10-995-561-365 (1-2188)

Qy 27 TrpGlyLeuAspThrMetArgGlnIleGlnValPheGluAspGluProAlaArgIleLys 46
Db 306 TGGGGGCTG-----GAAATGAGGCTTTAATTGTAAAGA 338

Qy 47 CysProLeuPheGluHisPheLeuLysPheAsnTyrSerThrAlaHisSerAlaGlyLeu 66
Db 339 TGTCTCT-----AGACAAAGAAACCTAGTTAC 365
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Qy	355	Arg-----TyrThrValGluLeuAlaCysGlyPheGlyAlaThrValLeuLeuVal	371
Db	1379	CATCATAGCATCTACTGCATAATTCGAGTAGT-----AGTGTATTTTAAATGCTAATC	1432
Qy	372	ValIleuIleValValTyrHisValTyrTrpLeuGluMetValLeuPheTyrArgAla	391
Db	1433	AATGTCTGTGTATCATCTCTAAANAATGTCTGTGATTTGAGGCCACTCTGCTCTCGAGAGAC	1492
Qy	392	HisPheGlyThrAspGluThrIleLeuAspGlyLysGluTyrAspIleTyrValSerTyr	411
Db	1493	ATAGCTAAACCTTACAAGCATAGGAAGTATGGAAGACTCTATGATGCTTATGTTGTCTAC	1552
Qy	412	AlaArgAsn-----AlaGluGluGluGluPheValLeuLeu	423
Db	1553	CCACGGAACTACAAATCCAGTACAGATGGGGCCAGTCGTGTAGACACTTTGTTTACCACG	1612
Qy	424	ThrLeuArgGlyValLeuGluAsnGluPheGlyTyrLysLeuCysIlePheAspArgAsp	443
Db	1613	ATTCTGCCTGATGTTCTTGAAATAAATGTGGCTATACCTTATGCATTTATGGGAGAGAT	1672
Qy	444	SerLeuProGlyGlyAsnThrValGluAlaValPheAspPheIleGlnArgSerArgArg	463
Db	1673	ATCTTACCTGGGAAAGATGTAGTCACTRCAGTGGAAACCAACATACGAAAGACGAGCGG	1732
Qy	464	MetIleValValLeuSerProAspTyrValThrGluLysSerIleSerMetLeuGluPhe	483
Db	1733	CACATTTCATCTGACCCCTCAGATCACTCAACAAVAGGAGTTTGC-----TAGCARGAC	1789
Qy	484	LysLeuGlyValMetCys-----GlnAsnSerIleAlaThrLysLeuIleValVal	500
Db	1790	GAGTTTCCCTCGCATGCTGCTCCCTCATCCAGAACGAC-----GCCAAGGTGATCTATT	1843
Qy	501	GluTyrArgProLeu-----GluHisProHisProGlyIle	512
Db	1844	GAGATGAGGCTCTGAGCGAGCTGGACATGCTCCAGGCTGAGCGGCTTCAGGACTCCCTC	1903
Qy	513	LeuGlnLeuLysGluSerValSerPheValSerTrpLysGlyGlu-----LysSer	529
Db	1904	MRCATCTTATGAAGTACAGGGGACCACTCAAGTGGAGGAGGACCACATTGCCAWTAA	1963
Qy	530	LysHisSerGlySerLysPheTrpLysAlaLeuArgLeuAlaLeuProLeuArgSer	548
Db	1964	AGGTCCCTGAATTCYAATTTCTGGAAGCAGCTGAGGTACCAATAGCTGTGCGCAAGC	2020
RESULT 15			
US-10-821-234-731			
; Sequence 731, Application US/10821234			
; Publication No. US20050255114A1			
; GENERAL INFORMATION:			
; APPLICANT: Labat, Ivan			
; APPLICANT: Stache-Crain, Birgit			
; APPLICANT: Andarmani, Susan			
; APPLICANT: Tang, Y. Tom			
; TITLE OF INVENTION: Methods for diagnosis and treatment of Preeclampsia			
; FILE REFERENCE: 821A			
; CURRENT APPLICATION NUMBER: US/10/821,234			
; CURRENT FILING DATE: 2004-04-07			
; PRIOR APPLICATION NUMBER: US 60/462,047			
; PRIOR FILING DATE: 2003-04-07			
; NUMBER OF SEQ ID NOS: 1704			
; SOFTWARE: pt_seq_genes Version 1.0			
; SEQ ID NO 731			
; LENGTH: 1197			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-10-821-234-731			
Alignment Scores:			
Pred. No.:		6 43e-15	Length: 1197
Score:		252.00	Matches: 79
Percent Similarity:		38.94%	Conservative: 53
Best Local Similarity:		23.30%	Mismatches: 146
Query Match:		6.87%	Indels: 62

Search completed: December 14, 2005, 18:42:33
Job time : 241 secs

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DB: 6 Gaps: 12
US-10-061-727-2 (1-687) x US-10-821-234-731 (1-1197)
Qy 20 AlaSerGluArgCysAspAspTyrGlyLeuAspThrMetArgGlnIleGlnValPheGlu 39
   |||:|
   |||:|
   |||:|
Db 70 GCTCCAGAGAGCTGCGGTTTCGTGGGAGGACATTACAAGCGGAGATTTCAGGCTG--GAA 126
   |||:|
   |||:|
   |||:|
Qy 40 AspGluProAlaArgIleLysCysProLeuPheGluHisPheLeuLysPheAsnTyrSer 59
   |||:|
   |||:|
   |||:|
Db 127 GGGAGAGCTGTAGCCCTGAGGTGCCCCCAGGTGCCCTACTGGTTGTGGGCTCTGTGAGC 186
   |||:|
   |||:|
   |||:|
Qy 60 ThrAlaHisSerAlaGlyLeuThrLeuIleTyrTrpThrArgGlnAspArgAspLeu 79
   |||:|
   |||:|
   |||:|
Db 187 CCCCCG-----ATCAACCTGACATGGCATAAATAATGACTCTGTAGGACGGTC 234
   |||:|
   |||:|
   |||:|
Qy 80 -----GluGluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAsp 97
   |||:|
   |||:|
   |||:|
Db 235 CCAGGAGAGAA-----GAGACACGGATGTGGGCCAGGACGGT 273
   |||:|
   |||:|
   |||:|
Qy 98 ValLeuTrpPheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArg 117
   |||:|
   |||:|
   |||:|
Db 274 GCTCTGTGGCTTCTGCCAGCCTTCAGGAGGACTCTGGCACCTACGTCCTGCACCTACTAGA 333
   |||:|
   |||:|
   |||:|
Qy 118 AsnThrThrTyrCysSerLysValAlaPheProLeuGluValValGlnLysAspSerCys 137
   |||:|
   |||:|
   |||:|
Db 334 AATGCTTCTTACTGTGACAAATGTCATTGAGCTCAGAGTTTGTGAGAATACAGATGCT 393
   |||:|
   |||:|
   |||:|
Qy 138 PheAsnSerProMetLysLeuProValHisLysLeuTyrIleGluTyr----- 153
   |||:|
   |||:|
   |||:|
Db 394 TTC-----CTGCCG-----TTCATCTCATACCCGCAAAATTTTA 426
   |||:|
   |||:|
   |||:|
Qy 154 -----GlyIleGlnArgIleThrCysProAsnValAspGlyTyrPhePro 168
   |||:|
   |||:|
   |||:|
Db 427 ACCTTGTCAACCTCTGGGGTA-----TTAGTATGCCCTGACCTGAGTGAATTCACCCGT 480
   |||:|
   |||:|
   |||:|
Qy 169 SerSerValLysProThrIleThrTyrMetGlyCysTyrLysIleGlnAsnPheAsn 188
   |||:|
   |||:|
   |||:|
Db 481 GACAAAACCTGACGTGAAGATTCAATGGTACAAGGATTCTCTCTTTTGGATAAAGACAAT 540
   |||:|
   |||:|
   |||:|
Qy 189 AsnValIleProGluGlyMetAsnLeuSerPheLeuIle-----AlaLeuIleSer 205
   |||:|
   |||:|
   |||:|
Db 541 GAGAAATTTCTAAGTGTGAGGGGACCACCTACTTACTCGTACACGATGTGGCCTGGAA 600
   |||:|
   |||:|
   |||:|
Qy 206 AsnAsnGlyAsnTyrThrCysValValThrTyrProGluAsnGlyArgThrPheHisLeu 225
   |||:|
   |||:|
   |||:|
Db 601 GATGCTGGCTATTACCGCTGTCTGTCACATTGGCCCATGAAGGCCAGCAATACACATC 660
   |||:|
   |||:|
   |||:|
Qy 226 ThrArgThrLeuThrValLysValValGlySerProLysAsnAlaValProProValIle 245
   |||:|
   |||:|
   |||:|
Db 661 ACTAGGAGTATTGAGCTACGCATCAAGAAAAAAGAGAGACCATTCTCTGTGATCATT 720
   |||:|
   |||:|
   |||:|
Qy 246 HisSerProAsnAspHisValValTyrGluLysGluProGly-GluGluLeuLeuIlePr 265
   |||:|
   |||:|
   |||:|
Db 721 TC-CCCCCTCAAGACCATATCAGCTTCTCT-----GGGGTCAAGACTGACAAATCCC 770
   |||:|
   |||:|
   |||:|
Qy 265 oCysThrValTyrPheSerPheLeuMetAspSerArgAsnGluValTrpTrpThrIleAs 285
   |||:|
   |||:|
   |||:|
Db 771 GTGTAGGTGTTTCTGGGAACCGGCACACCCCTTAACCCATGCTGTGTGGTGGACGGCAA 830
   |||:|
   |||:|
   |||:|
Qy 285 pGlyLysLysProAspIleThrIleAspValThrIleAsnGluSerIleSerHisSe 305
   |||:|
   |||:|
   |||:|
Db 831 T-----GACCCCATAGAGAGCGCCTACCCGGGAGG 863
   |||:|
   |||:|
   |||:|
Qy 305 rArgThrGluAspGluThrArgThrGlnIle----- 315
   |||:|
   |||:|
   |||:|
Db 864 CCGCGTGACCGGGGCCAGCCAGGATATTCAGAAAAAATAAGAGAACTACATTGAAGT 923
   |||:|
   |||:|
   |||:|
Qy 316 -----LeuSerIleLysLysValThrSerGluAspLeuLysArgSerTyrValCys 332
   |||:|
   |||:|
   |||:|
Db 924 GCCATTGATTTTTCATCTGTCAAGAGAGGATTTGCACATGGATTTTAAATGT 978
   |||:|
   |||:|
   |||:|
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OM protein - protein search, using sw model

Run on: December 7, 2005, 13:26:36 ; Search time 26 Seconds
(without alignments)
2184.546 Million cell updates/sec

Title: US-10-061-727-2
Perfect score: 3669
Sequence: 1 MTLWCVVSLYFYGILOSDA.....SALAHHTDLSNNDFYIL 687

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/PCRTUS_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2586	70.5	570	2	US-08-991-944-2
2	2586	70.5	570	2	US-09-173-151A-36
3	2586	70.5	570	2	US-09-949-016-6184
4	2586	70.5	591	2	US-09-949-016-11319
5	2327.5	63.4	570	2	US-08-991-944-4
6	2327.5	63.4	570	2	US-09-173-151A-21
7	1937.5	52.8	915	2	US-10-282-162-52
8	1937.5	52.8	917	2	US-10-282-162-54
9	1937.5	52.8	917	2	US-10-282-162-56
10	1935	52.7	900	2	US-10-282-162-40
11	1935	52.7	902	2	US-10-282-162-42
12	1935	52.7	902	2	US-10-282-162-44
13	1930	52.6	910	2	US-09-313-942-28
14	1930	52.6	910	2	US-10-282-162-28
15	1833	50.0	900	2	US-10-282-162-34
16	1833	50.0	902	2	US-10-282-162-36
17	1833	50.0	902	2	US-10-282-162-38
18	1830	49.9	917	2	US-10-282-162-48
19	1830	49.9	917	2	US-10-282-162-50
20	1829	49.9	915	2	US-10-282-162-46
21	825	22.5	686	2	US-09-173-151A-4
22	800	21.8	579	2	US-09-173-151A-2
23	762.5	20.8	668	2	US-09-173-151A-35
24	528	14.4	541	1	US-08-604-333-2
25	528	14.4	541	2	US-09-110-618-2
26	528	14.4	541	2	US-09-173-151A-28
27	528	14.4	541	2	US-09-578-178-2

28	528	14.4	541	2	US-09-577-806-2	Sequence 2, Appli
29	528	14.4	541	2	US-09-621-502-4	Sequence 4, Appli
30	528	14.4	541	2	US-09-949-002-360	Sequence 360, App
31	528	14.4	546	2	US-09-949-002-489	Sequence 489, App
32	520	14.2	521	2	US-08-996-338-20	Sequence 20, Appl
33	520	14.2	521	2	US-09-556-972-20	Sequence 20, Appl
34	496	13.5	555	2	US-09-173-151A-32	Sequence 32, Appl
35	484.5	13.2	576	1	US-07-821-716-4	Sequence 4, Appli
36	484.5	13.2	576	1	US-08-381-603-4	Sequence 4, Appli
37	484.5	13.2	576	1	US-08-924-376-4	Sequence 4, Appli
38	484.5	13.2	576	2	US-08-685-212-4	Sequence 4, Appli
39	484.5	13.2	576	2	US-09-173-151A-30	Sequence 30, Appli
40	484.5	13.2	576	2	US-08-466-932A-4	Sequence 4, Appli
41	484.5	13.2	576	4	PCT-US94-02414-4	Sequence 4, Appli
42	484.5	13.2	576	4	PCT-US96-08899-4	Sequence 4, Appli
43	479	13.1	537	1	US-08-604-333-4	Sequence 4, Appli
44	479	13.1	537	2	US-09-110-618-4	Sequence 4, Appli
45	479	13.1	537	2	US-09-173-151A-29	Sequence 29, Appli

ALIGNMENTS

RESULT 1
US-08-991-944-2
; Sequence 2, Application US/08991944
; Patent No. 6280955
; GENERAL INFORMATION:
; APPLICANT: Cao, Zhaodan
; TITLE OF INVENTION: Interleukin-1 Receptor Accessory Proteins,
; TITLE OF INVENTION: Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 75 DENISE DRIVE
; CITY: HILLSBOROUGH
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94010
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/991,944
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-014
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 343-4341
; TELEFAX: (650) 343-4342
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 570 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-991-944-2

Query Match 70.5%; Score 2586; DB 2; Length 570;
Best Local Similarity 85.3%; Pred. No. 7.8e-244;
Matches 488; Conservative 35; Mismatches 37; Indels 12; Gaps 4;

Oy	1	MTLWCVVSLYFYGILOSDASERCDDGLDMRQIQVFEDEPARIKCPLEFHFLEKFNYST	60
Db	1	MTLWCVVSLYFYGILOSDASERCDDGLDMRQIQVFEDEPARIKCPLEFHFLEKFNYST	60
Oy	61	AHSAGLTLLIYWTQRDLDEEPINFRPLPENRISKEKDVLMFRPTLLNDTGYTCLMRTWT	120

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Db 61 AHSAGLTLIWTQRDRLEPINFRLPENRISKEKOVLMFRPTLLNDTNGYTCMLRNTT 120
Qy 121 YCSKVAFFLEVQKDSFNSPMKLPVHKLYIEYGIQRIITCPNVDPGYPSSVKPTITWYMG 180
Db 121 YCSKVAFFLEVQKDSFNSPMKLPVHKLYIEYGIQRIITCPNVDPGYPSSVKPTITWYMG 180
Qy 181 CYKIQNFNNVPEGMNLSFLIALISNNGNYTCVVTYPENGRTFHLTRTLTKVVGSPKNA 240
Db 181 CYKIQNFNNVPEGMNLSFLIALISNNGNYTCVVTYPENGRTFHLTRTLTKVVGSPKNA 240
Qy 241 VPPVHSNDHVYVEKEPGEELLIPCTVYFSLMDSRNEVWMTIDGKKPDDITIDVTINE 300
Db 241 VPPVHSNDHVYVEKEPGEELLIPCTVYFSLMDSRNEVWMTIDGKKPDDITIDVTINE 300
Qy 301 SISHSRTEDETRTQILSIKKVTSDDLKRSYVCHARSAGKGEVAKAOKVQKVPAPRYTVEL 360
Db 301 SISHSRTEDETRTQILSIKKVTSDDLKRSYVCHARSAGKGEVAKAOKVQKVPAPRYTVEL 360
Qy 361 ACGFGATVLLVILVIVVHYVWLEWLVFYRAHFGTDETLIDGKEYDIYVSYARNAEBEFP 420
Db 361 ACGFGATVLLVILVIVVHYVWLEWLVFYRAHFGTDETLIDGKEYDIYVSYARNAEBEFP 420
Qy 421 VLLTLRGVLENEFGYKLCIFDRDSLPGGNTVEAVDFDFTQSRRMIVLSPDYVTEKSISM 480
Db 421 VLLTLRGVLENEFGYKLCIFDRDSLPGGNTVEAVDFDFTQSRRMIVLSPDYVTEKSISM 480
Qy 481 LEFLKGVMCQNSIATK----LIVVEYRPLEHPHFGILQLKES---VSFVSWKGEKSKHSG 533
Db 481 LELKAGL---ENMASRGNINVLQYKAVKETK--VKELKRAKTVLTVIKWGEKSKYPQ 535
Qy 534 SKFWKALRLALPLRSLASGWNESCSQSDI 565
Db 536 GRFWKQLQVAMPVKSPRRSSDQGLSYSSL 567
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RESULT 2

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US-09-173-151A-36
; Sequence 36, Application US/09173151A
; Patent No. 6326472
; GENERAL INFORMATION:
; APPLICANT: Timans, Jacqueline C.
; APPLICANT: Debets, Johannes Eduard Maria
; APPLICANT: Antonius
; APPLICANT: Sana, Theodore R.
; APPLICANT: Bazan, J. Fernando
; APPLICANT: Kastelein, Robert A.
; TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and Methods
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/173.151A
; FILING DATE: 14-OCT-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/065,776
; FILING DATE: 17-NOV-1997
; APPLICATION DATA:
; APPLICATION NUMBER: US 60/078,008
; FILING DATE: 12-MAR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/081,883
; FILING DATE: 15-APR-1998
```

```
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/095,987
; FILING DATE: 10-AUG-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/078,416
; FILING DATE: 18-MAR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/062,066
; FILING DATE: 15-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0767X
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)852-9196
; TELEFAX: (650)496-1200
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 570 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-173-151A-36
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Query Match 70.5%; Score 2586; DB 2; Length 570;
Best Local Similarity 85.3%; Pred. No. 7.8e-244;
Matches 488; Conservative 35; Mismatches 37; Indels 12; Gaps 4;

Qy 1 MTLWCVSLYFYGILOSASERCDDWGLDMRQIQVFEDEPARIKCPLFEHFLKFNYST 60
Db 1 MTLWCVSLYFYGILOSASERCDDWGLDMRQIQVFEDEPARIKCPLFEHFLKFNYST 60
Qy 61 AHSAGLTLIWTQRDRDLLEPINFRLPENRISKEKOVLMFRPTLLNDTNGYTCMLRNTT 120
Db 61 AHSAGLTLIWTQRDRDLLEPINFRLPENRISKEKOVLMFRPTLLNDTNGYTCMLRNTT 120
Qy 121 YCSKVAFFLEVQKDSFNSPMKLPVHKLYIEYGIQRIITCPNVDPGYPSSVKPTITWYMG 180
Db 121 YCSKVAFFLEVQKDSFNSPMKLPVHKLYIEYGIQRIITCPNVDPGYPSSVKPTITWYMG 180
Qy 181 CYKIQNFNNVPEGMNLSFLIALISNNGNYTCVVTYPENGRTFHLTRTLTKVVGSPKNA 240
Db 181 CYKIQNFNNVPEGMNLSFLIALISNNGNYTCVVTYPENGRTFHLTRTLTKVVGSPKNA 240
Qy 241 VPPVHSNDHVYVEKEPGEELLIPCTVYFSLMDSRNEVWMTIDGKKPDDITIDVTINE 300
Db 241 VPPVHSNDHVYVEKEPGEELLIPCTVYFSLMDSRNEVWMTIDGKKPDDITIDVTINE 300
Qy 301 SISHSRTEDETRTQILSIKKVTSDDLKRSYVCHARSAGKGEVAKAOKVQKVPAPRYTVEL 360
Db 301 SISHSRTEDETRTQILSIKKVTSDDLKRSYVCHARSAGKGEVAKAOKVQKVPAPRYTVEL 360
Qy 361 ACGFGATVLLVILVIVVHYVWLEWLVFYRAHFGTDETLIDGKEYDIYVSYARNAEBEFP 420
Db 361 ACGFGATVLLVILVIVVHYVWLEWLVFYRAHFGTDETLIDGKEYDIYVSYARNAEBEFP 420
Qy 421 VLLTLRGVLENEFGYKLCIFDRDSLPGGNTVEAVDFDFTQSRRMIVLSPDYVTEKSISM 480
Db 421 VLLTLRGVLENEFGYKLCIFDRDSLPGGNTVEAVDFDFTQSRRMIVLSPDYVTEKSISM 480
Qy 481 LEFLKGVMCQNSIATK----LIVVEYRPLEHPHFGILQLKES---VSFVSWKGEKSKHSG 533
Db 481 LELKAGL---ENMASRGNINVLQYKAVKETK--VKELKRAKTVLTVIKWGEKSKYPQ 535
Qy 534 SKFWKALRLALPLRSLASGWNESCSQSDI 565
Db 536 GRFWKQLQVAMPVKSPRRSSDQGLSYSSL 567
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RESULT 3

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US-09-949-016-6184
; Sequence 6184, Application US/09949016
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Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6184
LENGTH: 570
TYPE: PRT
ORGANISM: Human
US-09-949-016-6184

Query Match 70.5%; Score 2586; DB 2; Length 570;
Best Local Similarity 85.3%; Pred. No. 7.8e-244;
Matches 488; Conservative 35; Mismatches 37; Indels 12; Gaps 4;
QY 1 MTLWCVSLYFYGILQSDASERCDWGLDTRQIQVFEDEPARIKCPLFEHFLKFNYST 60
Db 1 MTLWCVSLYFYGILQSDASERCDWGLDTRQIQVFEDEPARIKCPLFEHFLKFNYST 60
QY 61 AHSAGTLIYWTRQDRDLLEPINFRLPENRISKEKDVLPFRPTLLNDTNGYTCMLRNTT 120
Db 61 AHSAGTLIYWTRQDRDLLEPINFRLPENRISKEKDVLPFRPTLLNDTNGYTCMLRNTT 120
QY 121 YCSKVAFLVQKDSFCNSPMKLPVHKLYIEYGQRTICPNVDGYFPSSVKPTITWYMG 180
Db 121 YCSKVAFLVQKDSFCNSPMKLPVHKLYIEYGQRTICPNVDGYFPSSVKPTITWYMG 180
QY 181 CYKIQNFNNVIPEGNNLSFLIALISNNGNYTCVVTYPENGRTHLTRLTVKVVGSPKNA 240
Db 181 CYKIQNFNNVIPEGNNLSFLIALISNNGNYTCVVTYPENGRTHLTRLTVKVVGSPKNA 240
QY 241 VPPVHSPNDHVYKEPGEELLIPCTVYFSLMDSRNEVWMTIDGKPPDDITIDVTINE 300
Db 241 VPPVHSPNDHVYKEPGEELLIPCTVYFSLMDSRNEVWMTIDGKPPDDITIDVTINE 300
QY 301 SISHSRTEDETRTQILSIKKVTSDDLKRSYVCHARSASAKGEVAKAOKVPAPRYTVEL 360
Db 301 SISHSRTEDETRTQILSIKKVTSDDLKRSYVCHARSASAKGEVAKAOKVPAPRYTVEL 360
QY 361 ACGGATVLLVILVYVHVWLEWLVFYRAHFGTDEILDGKEYDIYVSVARNABEEF 420
Db 361 ACGGATVLLVILVYVHVWLEWLVFYRAHFGTDEILDGKEYDIYVSVARNABEEF 420
QY 421 VLLTLRGVLENEFGYKLCIFDRDSLPGGIVTDETLSPQRSRRMIVLSPDYVTEKISM 480
Db 421 VLLTLRGVLENEFGYKLCIFDRDSLPGGIVTDETLSPQRSRRMIVLSPDYVTEKISM 480
QY 481 LEFLKGLVMCONSIA TK----LIVVEYRPLEHPHPIQLKES---VSFVSWKGEKSKHSG 533
Db 481 LELKAGL---ENMASRGNINVLQYKAVKETK--VKELKRAKTVLTVIKWGEKSKYPQ 535
QY 534 SKFWKALRALPLRLSLASSGNESCSCSSQSDI 565
Db 536 GRFWKQLQVAMPVKSPRRSSDEQGLSYSSL 567

RESULT 4
US-09-949-016-11319
Sequence 11319, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11319
LENGTH: 591
TYPE: PRT
ORGANISM: Human
US-09-949-016-11319

Query Match 70.5%; Score 2586; DB 2; Length 591;
Best Local Similarity 85.3%; Pred. No. 8.3e-244;
Matches 488; Conservative 35; Mismatches 37; Indels 12; Gaps 4;
QY 1 MTLWCVSLYFYGILQSDASERCDWGLDTRQIQVFEDEPARIKCPLFEHFLKFNYST 60
Db 22 MTLWCVSLYFYGILQSDASERCDWGLDTRQIQVFEDEPARIKCPLFEHFLKFNYST 81
QY 61 AHSAGTLIYWTRQDRDLLEPINFRLPENRISKEKDVLPFRPTLLNDTNGYTCMLRNTT 120
Db 82 AHSAGTLIYWTRQDRDLLEPINFRLPENRISKEKDVLPFRPTLLNDTNGYTCMLRNTT 141
QY 121 YCSKVAFLVQKDSFCNSPMKLPVHKLYIEYGQRTICPNVDGYFPSSVKPTITWYMG 180
Db 142 YCSKVAFLVQKDSFCNSPMKLPVHKLYIEYGQRTICPNVDGYFPSSVKPTITWYMG 201
QY 181 CYKIQNFNNVIPEGNNLSFLIALISNNGNYTCVVTYPENGRTHLTRLTVKVVGSPKNA 240
Db 202 CYKIQNFNNVIPEGNNLSFLIALISNNGNYTCVVTYPENGRTHLTRLTVKVVGSPKNA 261
QY 241 VPPVHSPNDHVYKEPGEELLIPCTVYFSLMDSRNEVWMTIDGKPPDDITIDVTINE 300
Db 262 VPPVHSPNDHVYKEPGEELLIPCTVYFSLMDSRNEVWMTIDGKPPDDITIDVTINE 321
QY 301 SISHSRTEDETRTQILSIKKVTSDDLKRSYVCHARSASAKGEVAKAOKVPAPRYTVEL 360
Db 322 SISHSRTEDETRTQILSIKKVTSDDLKRSYVCHARSASAKGEVAKAOKVPAPRYTVEL 381
QY 361 ACGGATVLLVILVYVHVWLEWLVFYRAHFGTDEILDGKEYDIYVSVARNABEEF 420
Db 382 ACGGATVLLVILVYVHVWLEWLVFYRAHFGTDEILDGKEYDIYVSVARNABEEF 441
QY 421 VLLTLRGVLENEFGYKLCIFDRDSLPGGIVTDETLSPQRSRRMIVLSPDYVTEKISM 480
Db 442 VLLTLRGVLENEFGYKLCIFDRDSLPGGIVTDETLSPQRSRRMIVLSPDYVTEKISM 501
QY 481 LEFLKGLVMCONSIA TK----LIVVEYRPLEHPHPIQLKES---VSFVSWKGEKSKHSG 533
Db 502 LELKAGL---ENMASRGNINVLQYKAVKETK--VKELKRAKTVLTVIKWGEKSKYPQ 556
QY 534 SKFWKALRALPLRLSLASSGNESCSCSSQSDI 565
Db 557 GRFWKQLQVAMPVKSPRRSSDEQGLSYSSL 588

RESULT 5
US-08-991-944-4
Sequence 4, Application US/08991944
Patent No. 6280955
GENERAL INFORMATION:
APPLICANT: Cao, Zhaodan
TITLE OF INVENTION: Interleukin-1 Receptor Accessory Proteins,
Nucleic Acids and Methods
TITLE OF INVENTION: Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4


```

Qy 61 AHSAGLTLIYWTRQDRDLDEEPINFRLENRISKEKDVLPFRPTLLNDTGNVTCMLRNTT 120
Db 61 AHSAGLTLIYWTRQDRDLDEEPINFRLENRISKEKDVLPFRPTLLNDTGNVTCMLRNTT 120
Qy 121 YCSKVAFPLEVVKQDSCFNSPKMLPVHKLIEYGIQRTICPNVDGYFPSSVKPPTITWYMG 180
Db 121 YCSKVAFPLEVVKQDSCFNSPKMLPVHKLIEYGIQRTICPNVDGYFPSSVKPPTITWYMG 180
Qy 181 CYKIQNFNNVPEGMNLSFLIALISNNGNYTCVVYPENGRTFHLTRTLTKVVGSPKNA 240
Db 181 CYKIQNFNNVPEGMNLSFLIALISNNGNYTCVVYPENGRTFHLTRTLTKVVGSPKNA 240
Qy 241 VPPVIHSPNDHVYKEPGEELLIPCTVYFSLMDSRNEVWMTIDGKKPDDITIDVTINE 300
Db 241 CTEIVDFHNVLPEGMNLSFLIALISNNGNYTCVVYPENGRTFHLTRTLTKVVGSPKNA 240
Qy 300 SISHSRTEDETRTQILSIKKVTSDDLKRSYVCHARSAGEVAKAAKVKQKVPAPRYTVEL 360
Db 300 SISHSRTEDETRTQILSIKKVTSDDLKRSYVCHARSAGEVAKAAKVKQKVPAPRYTVEL 360
Qy 361 ACAGFATVLLVILVYVHVWLEMLFYRAHFGTDETLIDGKEYDIYVSARNVEEEF 420
Db 361 ACAGFATVLLVILVYVHVWLEMLFYRAHFGTDETLIDGKEYDIYVSARNVEEEF 420
Qy 421 VLLTLRGVLENEFGYKLCIFDRSLPGGNTVEAVPDFIORSRMIIVLSPDYVTEKSISM 480
Db 421 VLLTLRGVLENEFGYKLCIFDRSLPGGNTVEAVPDFIORSRMIIVLSPDYVTEKSISM 480
Qy 481 LEFKLVGMVCONSIAK-----LIVVEYRPLEPHPHQILQKES---VSFVSWKGEKSKHSG 533
Db 481 LELKAGL---ENMASRGINVILVQYKAVKDMK--VKELKRAKTVLTVIKWGEKSKYPQ 535
Qy 534 SKFWKALPLALPLRLSLSSASSGNES 558
Db 536 GRFWKQQLVAMPVKK---SPRWSSN 557

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RESULT 7

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US-10-282-162-52
; Sequence 52, Application US/10282162
; Patent No. 6927044
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; TITLE OF INVENTION: AND USING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282.162
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 52
; LENGTH: 915
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-282-162-52

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```

Query Match 52.8%; Score 1937.5; DB 2; Length 915;
Best Local Similarity 80.9%; Pred. No. 5.2e-180;
Matches 381; Conservative 11; Mismatches 34; Indels 45; Gaps 7;

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Qy 1 MTLWCVSVLYFYGILQSDASERCDDWGLDMRQIQVFEDEPARIKCPLEFHLKFNYST 60
Db 1 MVLWCVSVLYFYGILQSDASERCDDWGLDMRQIQVFEDEPARIKCPLEFHLKFNYST 60
Qy 61 AHSAGLTLIYWTRQDRDLDEEPINFRLENRISKEKDVLPFRPTLLNDTGNVTCMLRNTT 120
Db 61 AHSAGLTLIYWTRQDRDLDEEPINFRLENRISKEKDVLPFRPTLLNDTGNVTCMLRNTT 120

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Qy 121 YCSKVAFPLEVVKQDSCFNSPKMLPVHKLIEYGIQRTICPNVDGYFPSSVKPPTITWYMG 180
Db 121 YCSKVAFPLEVVKQDSCFNSPKMLPVHKLIEYGIQRTICPNVDGYFPSSVKPPTITWYMG 180
Qy 181 CYKIQNFNNVPEGMNLSFLIALISNNGNYTCVVYPENGRTFHLTRTLTKVVGSPKNA 240
Db 181 CYKIQNFNNVPEGMNLSFLIALISNNGNYTCVVYPENGRTFHLTRTLTKVVGSPKNA 240
Qy 241 VPPVIHSPNDHVYKEPGEELLIPCTVYFSLMDSRNEVWMTIDGKKPDDITIDVTINE 300
Db 241 VPPVIHSPNDHVYKEPGEELLIPCTVYFSLMDSRNEVWMTIDGKKPDDITIDVTINE 300
Qy 300 SISHSRTEDETRTQILSIKKVTSDDLKRSYVCHARSAGEVAKAAKVKQKVPAPRYTVEL 360
Db 300 SISHSRTEDETRTQILSIKKVTSDDLKRSYVCHARSAGEVAKAAKVKQKVPAPRYTVEL 360
Qy 361 ACAGF-----GATVLLVILVYVHVWLEMLFYRAHF----- 393
Db 361 GAARSCFRGRHYKREPRLEGEVALRCPQV-----PYWLWASVSPRINLTWHKNDARSATV 416
Qy 394 -GTDETL-----DG-----KEYDIYVSARNVEEEFVLLTLRGVLEN 431
Db 417 PGBETRMAQDQALWLLPALQEDSGTYVCTTRNASYCDKMSIELR-VFEN 466

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RESULT 8

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US-10-282-162-54
; Sequence 54, Application US/10282162
; Patent No. 6927044
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; TITLE OF INVENTION: AND USING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282.162
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 54
; LENGTH: 917
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-282-162-54

```

```

Query Match 52.8%; Score 1937.5; DB 2; Length 917;
Best Local Similarity 80.9%; Pred. No. 5.3e-180;
Matches 381; Conservative 11; Mismatches 34; Indels 45; Gaps 7;

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Qy 1 MTLWCVSVLYFYGILQSDASERCDDWGLDMRQIQVFEDEPARIKCPLEFHLKFNYST 60
Db 1 MVLWCVSVLYFYGILQSDASERCDDWGLDMRQIQVFEDEPARIKCPLEFHLKFNYST 60
Qy 61 AHSAGLTLIYWTRQDRDLDEEPINFRLENRISKEKDVLPFRPTLLNDTGNVTCMLRNTT 120
Db 61 AHSAGLTLIYWTRQDRDLDEEPINFRLENRISKEKDVLPFRPTLLNDTGNVTCMLRNTT 120
Qy 121 YCSKVAFPLEVVKQDSCFNSPKMLPVHKLIEYGIQRTICPNVDGYFPSSVKPPTITWYMG 180
Db 121 YCSKVAFPLEVVKQDSCFNSPKMLPVHKLIEYGIQRTICPNVDGYFPSSVKPPTITWYMG 180
Qy 181 CYKIQNFNNVPEGMNLSFLIALISNNGNYTCVVYPENGRTFHLTRTLTKVVGSPKNA 240
Db 181 CYKIQNFNNVPEGMNLSFLIALISNNGNYTCVVYPENGRTFHLTRTLTKVVGSPKNA 240
Qy 241 VPPVIHSPNDHVYKEPGEELLIPCTVYFSLMDSRNEVWMTIDGKKPDDITIDVTINE 300
Db 241 VPPVIHSPNDHVYKEPGEELLIPCTVYFSLMDSRNEVWMTIDGKKPDDITIDVTINE 300
Qy 301 SISHSRTEDETRTQILSIKKVTSDDLKRSYVCHARSAGEVAKAAKVKQKVPAPRYTVEL 360

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Db 301 SISHSRTEDETRQILSIKKVTSDDLKRSVCHARSAGKGEVAKAAVKQKVPAPRYTVHT 360
Qy 361 -----ACGF-----GATVLLVILVVVHVHVMLEVLVYRAHF 393
Db 361 GAARSCFRGRHYKREFRLEGEPVALRCPOV-----PYWLWASVSPRINLTWHKNDARSATV 416
Qy 394 -GTDETEL-----DG-----KEYDIYVSARNAESEEFVLLTLRGVLEN 431
Db 417 PGBEETRMWAQDGAALLPALQEDSGTYVCTTRNASYCDKMSIELR-VFEN 466

RESULT 9
US-10-282-162-56
; Sequence 56, Application US/10282162
; Patent No. 6927044
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282,162
; PRIOR FILING DATE: 2002-10-28
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 56
; LENGTH: 917
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-282-162-56

Query Match 52.8%; Score 1937, 5; DB 2; Length 917;
Best Local Similarity 80.9%; Pred. No. 5.3e-180;
Matches 381; Conservative 11; Mismatches 34; Indels 45; Gaps 7;

Qy 1 MTLWCVSLYFYGILQSDASERCDDWGLDTMRQIQVFEDEPARIKCPLEFHEFLKFNYS 60
Db 1 MVLWCVSLYFYGILQSDASERCDDWGLDTMRQIQVFEDEPARIKCPLEFHEFLKFNYS 60
Qy 61 AHSAGTLIYWTRQDRDLDEEPINFRLPENRISKEDVLFWRPTLLNDTGNITCMLRNTT 120
Db 61 AHSAGTLIYWTRQDRDLDEEPINFRLPENRISKEDVLFWRPTLLNDTGNITCMLRNTT 120
Qy 121 YCSKVAPPLEVQKDCSFNSPMKLPVHKLYIEYGIORITCPNVDGYFPSSVKPTITWYMG 180
Db 121 YCSKVAPPLEVQKDCSFNSPMKLPVHKLYIEYGIORITCPNVDGYFPSSVKPTITWYMG 180
Qy 181 CYKIQNFNNVPIEGMNLSPFLIALISNNGNYTCVVTYPENGRTFHLTRTLTKVVGSPKNA 240
Db 181 CYKIQNFNNVPIEGMNLSPFLIALISNNGNYTCVVTYPENGRTFHLTRTLTKVVGSPKNA 240
Qy 241 VPPVHSPNDHVVEKPGSELLIPCTVYPSFLMDSRNEVWWTIDGKKPDDITIDVTINE 300
Db 241 VPPVHSPNDHVVEKPGSELLIPCTVYPSFLMDSRNEVWWTIDGKKPDDITIDVTINE 300
Qy 301 SISHSRTEDETRQILSIKKVTSDDLKRSVCHARSAGKGEVAKAAVKQKVPAPRYTVEL 360
Db 301 SISHSRTEDETRQILSIKKVTSDDLKRSVCHARSAGKGEVAKAAVKQKVPAPRYTVHT 360
Qy 361 -----ACGF-----GATVLLVILVVVHVHVMLEVLVYRAHF 393
Db 361 GAARSCFRGRHYKREFRLEGEPVALRCPOV-----PYWLWASVSPRINLTWHKNDARSATV 416
Qy 394 -GTDETEL-----DG-----KEYDIYVSARNAESEEFVLLTLRGVLEN 431
Db 417 PGBEETRMWAQDGAALLPALQEDSGTYVCTTRNASYCDKMSIELR-VFEN 466

RESULT 10

US-10-282-162-40
; Sequence 40, Application US/10282162
; Patent No. 6927044
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282,162
; PRIOR FILING DATE: 2002-10-28
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 40
; LENGTH: 900
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-282-162-40

Query Match 52.7%; Score 1935; DB 2; Length 900;
Best Local Similarity 99.7%; Pred. No. 9e-180;
Matches 358; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MTLWCVSLYFYGILQSDASERCDDWGLDTMRQIQVFEDEPARIKCPLEFHEFLKFNYS 60
Db 1 MVLWCVSLYFYGILQSDASERCDDWGLDTMRQIQVFEDEPARIKCPLEFHEFLKFNYS 60
Qy 61 AHSAGTLIYWTRQDRDLDEEPINFRLPENRISKEDVLFWRPTLLNDTGNITCMLRNTT 120
Db 61 AHSAGTLIYWTRQDRDLDEEPINFRLPENRISKEDVLFWRPTLLNDTGNITCMLRNTT 120
Qy 121 YCSKVAPPLEVQKDCSFNSPMKLPVHKLYIEYGIORITCPNVDGYFPSSVKPTITWYMG 180
Db 121 YCSKVAPPLEVQKDCSFNSPMKLPVHKLYIEYGIORITCPNVDGYFPSSVKPTITWYMG 180
Qy 181 CYKIQNFNNVPIEGMNLSPFLIALISNNGNYTCVVTYPENGRTFHLTRTLTKVVGSPKNA 240
Db 181 CYKIQNFNNVPIEGMNLSPFLIALISNNGNYTCVVTYPENGRTFHLTRTLTKVVGSPKNA 240
Qy 241 VPPVHSPNDHVVEKPGSELLIPCTVYPSFLMDSRNEVWWTIDGKKPDDITIDVTINE 300
Db 241 VPPVHSPNDHVVEKPGSELLIPCTVYPSFLMDSRNEVWWTIDGKKPDDITIDVTINE 300
Qy 301 SISHSRTEDETRQILSIKKVTSDDLKRSVCHARSAGKGEVAKAAVKQKVPAPRYTVE 359
Db 301 SISHSRTEDETRQILSIKKVTSDDLKRSVCHARSAGKGEVAKAAVKQKVPAPRYTVE 359

RESULT 11
US-10-282-162-42
; Sequence 42, Application US/10282162
; Patent No. 6927044
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282,162
; PRIOR FILING DATE: 2002-10-28
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 42
; LENGTH: 902
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-282-162-42

Query Match 52.7%; Score 1935; DB 2; Length 902;
 Best Local Similarity 99.7%; Pred. No. 9e-180;
 Matches 358; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTLWCVSLYFYGILQSDASERCDWGLDTRMQIQVFDEPARIKCPLFEHFLKFNYST 60
 DB 1 MVLWCVSLYFYGILQSDASERCDWGLDTRMQIQVFDEPARIKCPLFEHFLKFNYST 60

QY 61 AHSAGTLIWTWTRQDRDLPEPINFRLPENRISKEKDVLFWRPRTLNDGTNYTCMLRNTT 120
 DB 61 AHSAGTLIWTWTRQDRDLPEPINFRLPENRISKEKDVLFWRPRTLNDGTNYTCMLRNTT 120

QY 121 YCSKVAFFLEVQKQSCFNSPKMLPVHKLIEYGIQRTICPNVDGYFPSSVKPPTITWYMG 180
 DB 121 YCSKVAFFLEVQKQSCFNSPKMLPVHKLIEYGIQRTICPNVDGYFPSSVKPPTITWYMG 180

QY 181 CYKIQNFNNVIPEGNNLSFLIALISNNGNYTCVVTYPENGRFTHLTRLTVKVGSPKNA 240
 DB 181 CYKIQNFNNVIPEGNNLSFLIALISNNGNYTCVVTYPENGRFTHLTRLTVKVGSPKNA 240

QY 241 VPPVHSPNDHVYKEPGEELLIPCTVYFSLMDSRNEVWMTIDGKPPDDITIDVTINE 300
 DB 241 VPPVHSPNDHVYKEPGEELLIPCTVYFSLMDSRNEVWMTIDGKPPDDITIDVTINE 300

QY 301 SISHSRTEDETRTQILSIKKVTSDELKRSYVCHARSAGEVAKAAKVKQVPAPRYTVE 359
 DB 301 SISHSRTEDETRTQILSIKKVTSDELKRSYVCHARSAGEVAKAAKVKQVPAPRYTVE 359

RESULT 12
 US-10-282-162-44
 ; Sequence 44, Application US/10282162
 ; Patent No. 6927044
 ; GENERAL INFORMATION:
 ; APPLICANT: REGENERON PHARMACEUTICALS, INC.
 ; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
 ; FILE REFERENCE: REG 203-B-US
 ; CURRENT APPLICATION NUMBER: US/10/282,162
 ; PRIOR FILING DATE: 2002-10-28
 ; PRIOR FILING DATE: 1999-09-22
 ; PRIOR FILING DATE: 1999-09-22
 ; NUMBER OF SEQ ID NOS: 56
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 44
 ; LENGTH: 902
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-282-162-44

Query Match 52.7%; Score 1935; DB 2; Length 902;
 Best Local Similarity 99.7%; Pred. No. 9e-180;
 Matches 358; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTLWCVSLYFYGILQSDASERCDWGLDTRMQIQVFDEPARIKCPLFEHFLKFNYST 60
 DB 1 MVLWCVSLYFYGILQSDASERCDWGLDTRMQIQVFDEPARIKCPLFEHFLKFNYST 60

QY 61 AHSAGTLIWTWTRQDRDLPEPINFRLPENRISKEKDVLFWRPRTLNDGTNYTCMLRNTT 120
 DB 61 AHSAGTLIWTWTRQDRDLPEPINFRLPENRISKEKDVLFWRPRTLNDGTNYTCMLRNTT 120

QY 121 YCSKVAFFLEVQKQSCFNSPKMLPVHKLIEYGIQRTICPNVDGYFPSSVKPPTITWYMG 180
 DB 121 YCSKVAFFLEVQKQSCFNSPKMLPVHKLIEYGIQRTICPNVDGYFPSSVKPPTITWYMG 180

QY 181 CYKIQNFNNVIPEGNNLSFLIALISNNGNYTCVVTYPENGRFTHLTRLTVKVGSPKNA 240
 DB 181 CYKIQNFNNVIPEGNNLSFLIALISNNGNYTCVVTYPENGRFTHLTRLTVKVGSPKNA 240

QY 241 VPPVHSPNDHVYKEPGEELLIPCTVYFSLMDSRNEVWMTIDGKPPDDITIDVTINE 300
 DB 241 VPPVHSPNDHVYKEPGEELLIPCTVYFSLMDSRNEVWMTIDGKPPDDITIDVTINE 300

QY 301 SISHSRTEDETRTQILSIKKVTSDELKRSYVCHARSAGEVAKAAKVKQVPAPRYTVE 359
 DB 301 SISHSRTEDETRTQILSIKKVTSDELKRSYVCHARSAGEVAKAAKVKQVPAPRYTVE 359

RESULT 13
 US-09-313-942-28
 ; Sequence 28, Application US/09313942
 ; Patent No. 6472179
 ; GENERAL INFORMATION:
 ; APPLICANT: REGENERON PHARMACEUTICALS, INC.
 ; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
 ; FILE REFERENCE: REG 203-A
 ; CURRENT FILING DATE: 1999-05-19
 ; PRIOR FILING DATE: 09/313,942
 ; PRIOR FILING DATE: 1999-05-19
 ; PRIOR APPLICATION NUMBER: 60/101,858
 ; PRIOR FILING DATE: 1998-09-25
 ; NUMBER OF SEQ ID NOS: 32
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 28
 ; LENGTH: 910
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-313-942-28

Query Match 52.6%; Score 1930; DB 2; Length 910;
 Best Local Similarity 99.7%; Pred. No. 2.8e-179;
 Matches 357; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTLWCVSLYFYGILQSDASERCDWGLDTRMQIQVFDEPARIKCPLFEHFLKFNYST 60
 DB 1 MVLWCVSLYFYGILQSDASERCDWGLDTRMQIQVFDEPARIKCPLFEHFLKFNYST 60

QY 61 AHSAGTLIWTWTRQDRDLPEPINFRLPENRISKEKDVLFWRPRTLNDGTNYTCMLRNTT 120
 DB 61 AHSAGTLIWTWTRQDRDLPEPINFRLPENRISKEKDVLFWRPRTLNDGTNYTCMLRNTT 120

QY 121 YCSKVAFFLEVQKQSCFNSPKMLPVHKLIEYGIQRTICPNVDGYFPSSVKPPTITWYMG 180
 DB 121 YCSKVAFFLEVQKQSCFNSPKMLPVHKLIEYGIQRTICPNVDGYFPSSVKPPTITWYMG 180

QY 181 CYKIQNFNNVIPEGNNLSFLIALISNNGNYTCVVTYPENGRFTHLTRLTVKVGSPKNA 240
 DB 181 CYKIQNFNNVIPEGNNLSFLIALISNNGNYTCVVTYPENGRFTHLTRLTVKVGSPKNA 240

QY 241 VPPVHSPNDHVYKEPGEELLIPCTVYFSLMDSRNEVWMTIDGKPPDDITIDVTINE 300
 DB 241 VPPVHSPNDHVYKEPGEELLIPCTVYFSLMDSRNEVWMTIDGKPPDDITIDVTINE 300

QY 301 SISHSRTEDETRTQILSIKKVTSDELKRSYVCHARSAGEVAKAAKVKQVPAPRYTVE 358
 DB 301 SISHSRTEDETRTQILSIKKVTSDELKRSYVCHARSAGEVAKAAKVKQVPAPRYTVE 358

RESULT 14
 US-10-282-162-28
 ; Sequence 28, Application US/10282162
 ; Patent No. 6927044
 ; GENERAL INFORMATION:
 ; APPLICANT: REGENERON PHARMACEUTICALS, INC.
 ; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
 ; FILE REFERENCE: REG 203-B-US
 ; CURRENT APPLICATION NUMBER: US/10/282,162
 ; CURRENT FILING DATE: 2002-10-28
 ; PRIOR APPLICATION NUMBER: 09/787,835

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; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 910
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-282-162-28

Query Match      52.6%; Score 1930; DB 2; Length 910;
Best Local Similarity 99.7%; Pred. No. 2.8e-179;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MTLWCVVSLFYGYILQSDASERCDWGLDTRMQIQVFEDEPARIKCPLEFHFLLKFNYS 60
Db 1 MVLWCVVSLFYGYILQSDASERCDWGLDTRMQIQVFEDEPARIKCPLEFHFLLKFNYS 60

Qy 61 AHSAGLLIYWTRQDRDLDEPINFRLPENRISKEKDVLPFRPTLLNDTGNVTCMLRNTT 120
Db 61 AHSAGLLIYWTRQDRDLDEPINFRLPENRISKEKDVLPFRPTLLNDTGNVTCMLRNTT 120

Qy 121 YCSKVAAPLEVVQKSCFNSPMKLPVHKLYIEYGIQRIITCPNVGDYFPSSVKPTITWYMG 180
Db 121 YCSKVAAPLEVVQKSCFNSPMKLPVHKLYIEYGIQRIITCPNVGDYFPSSVKPTITWYMG 180

Qy 181 CYKIQNFNNVIPEGNNLSFLIALISNNGNYTCVVYTPENGRTFHLTRTLTKVVGSPKNA 240
Db 181 CYKIQNFNNVIPEGNNLSFLIALISNNGNYTCVVYTPENGRTFHLTRTLTKVVGSPKNA 240

Qy 241 VPPVIHSPNDHVYVEKEPGBELLIPCTVYFSLMDSNEVWMTIDGKKPDDITIDVTINE 300
Db 241 VPPVIHSPNDHVYVEKEPGBELLIPCTVYFSLMDSNEVWMTIDGKKPDDITIDVTINE 300

Qy 301 SISHSRTEDETRTOILSIKKVTSDDLKRSYVCHARSAGEVAKAAVKQKVPAPRYTV 358
Db 301 SISHSRTEDETRTOILSIKKVTSDDLKRSYVCHARSAGEVAKAAVKQKVPAPRYTV 358

RESULT 15
US-10-282-162-34
; Sequence 34, Application US/10282162
; Patent No. 6927044
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282,162
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 34
; LENGTH: 900
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-282-162-34

Query Match      50.0%; Score 1833; DB 2; Length 900;
Best Local Similarity 100.0%; Pred. No. 8.6e-170;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 SERCDDWGLDTRMQIQVFEDEPARIKCPLEFHFLLKFNYSHTAHSAGLLIYWTRQDRDL 80
Db 333 SERCDDWGLDTRMQIQVFEDEPARIKCPLEFHFLLKFNYSHTAHSAGLLIYWTRQDRDL 392

Qy 81 EPINFRLPENRISKEKDVLPFRPTLLNDTGNVTCMLRNTTYCSKVAAPLEVVQKSCFNS 140
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Search completed: December 7, 2005, 13:34:28
Job time : 28 secs